SCORE - Version Listing for Application 10723361

| Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions |

This page displays a list of all versions submitted by applicant for this application. Each new submission is given a "version" number by date received.

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Summary of Information

Version Number	Version Date	Current Working Copy
1	Tue Aug 29 11:29:07 EDT 2006	N
2	Tue Aug 29 11:29:07 EDT 2006	N

SCORE 1.3   BuildDate: 12/06/2005

SCORE Search Results for Application 10723361

This page gives you a list of all the Search Results. Use this page to obtain specific Search Result information.

View version list for this application

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Item Listing Version# 1

Item Name	Download Content
us-10-723-361-3.oligo.rag	Download
us-10-723-361-3.oligo.rai	Download
us-10-723-361-3.oligo.rapbm	Download
us-10-723-361-3.oligo.rapbn	Download
us-10-723-361-3.oligo.rpr	Download
us-10-723-361-3.oligo.rup	Download
us-10-723-361-3.rag	Download
us-10-723-361-3.rai	Download
us-10-723-361-3.rapbm	Download
us-10-723-361-3.rapbn	Download
us-10-723-361-3.rge	Download
us-10-723-361-3.rng	Download
us-10-723-361-3.rni	Download
us-10-723-361-3.rnpbm	Download
us-10-723-361-3.rnpbn	Download
us-10-723-361-3.rpr	Download
us-10-723-361-3.rst	Download
us-10-723-361-3.rup	Download

SCORE Search Results for Application 10723361

This page gives you a list of all the Search Results. Use this page to obtain specific Search Result information.

View version list for this application

Item Listing Version# 2

Item Name	Download Content
us-10-723-361-3.rnpbm	Download

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2006, 06:19:16 ; Search time 2871 Seconds
                                             (without alignments)
                                             9354.615 Million cell updates/sec

Title: US-10-723-361-3
Perfect score: 13101
Sequence: 1 MAISSRLALWEQKIREEDKS..........PGTGRKDDDVASIMKKYLQK 2568

Scoring table: BLOSUM62
                   Xgapop 10.0 , Xgapext   0.5
                   Ygapop 10.0 , Ygapext   0.5
                   Fgapop 6.0 , Fgapext   7.0
                   Delop   6.0 , Delext   7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10723361/runat_26062006_061901_27734/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10723361_@CGN_1_1_1147_@runat_26062006_061901_27734 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_8:*
                   1: geneseqn1980s:*
                   2: geneseqn1990s:*
                   3: geneseqn2000s:*
                   4: geneseqn2001as:*
                   5: geneseqn2001bs:*
                   6: geneseqn2002as:*
                   7: geneseqn2002bs:*
                   8: geneseqn2003as:*
                   9: geneseqn2003bs:*
                   10: geneseqn2003cs:*
                   11: geneseqn2003ds:*
                   12: geneseqn2004as:*
                   13: geneseqn2004bs:*
                   14: geneseqn2005s:*
                   15: geneseqn2006s:*

          Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13101	100.0	7707	6	ABN00011	Abn00011 Human gen
2	13101	100.0	7707	13	ACN63101	Acn63101 Human GDM
3	13101	100.0	8117	6	ABN00010	Abn00010 Human gen
4	13101	100.0	8117	6	AAL46722	Aal46722 Human myo
5	13101	100.0	8117	13	ACN63100	Acn63100 Human GDM
6	10312.5	78.7	6470	8	ACC44301	Acc44301 Gene enco
7	7911	60.4	4916	6	ABN00013	Abn00013 Human gen
8	7911	60.4	4916	13	ACN63103	Acn63103 Human GDM
9	4799	36.6	2953	6	ABN00012	Abn00012 Human gen
10	4799	36.6	2953	13	ACN63102	Acn63102 Human GDM
11	3717.5	28.4	7597	12	ADN00356	Adn00356 Novel hum
12	3715	28.4	7557	8	AAD49607	Aad49607 Human cyt
13	3692	28.2	6165	14	ADV43366	Adv43366 Human psy
14	3640.5	27.8	6524	10	ABX70653	Abx70653 Human cDN
15	3421.5	26.1	7072	10	ADE15680	Ade15680 Human str
16	2626	20.0	1946	10	ADC30382	Adc30382 Human nov
17	2561	19.5	1736	11	ADM02296	Adm02296 Human cDN
18	2561	19.5	1736	14	AEC85226	Aec85226 Human cDN
19	2294	17.5	1314	6	ABN15675	Abn15675 Human gen
20	2294	17.5	1314	13	ACN78765	Acn78765 Human GDM
21	2243.5	17.1	4714	5	AAS72285	Aas72285 DNA encod
22	2243.5	17.1	4714	10	ADC32253	Adc32253 Human nov
23	2143.5	16.4	4941	4	ABL19103	Abl19103 Drosophil
24	2113.5	16.1	5121	4	ABL29055	Abl29055 Drosophil
25	2100	16.0	1465	4	ABA31219	Aba31219 Probe #96
26	2100	16.0	1465	4	AAK38261	Aak38261 Human bon
27	2095	16.0	1246	6	ABN15714	Abn15714 Human gen
28	2095	16.0	1246	13	ACN78804	Acn78804 Human GDM
29	1620	12.4	934	12	ACH91928	Ach91928 Human gen
30	1456	11.1	853	4	ABA64603	Aba64603 Human foe
31	1456	11.1	853	4	AAI44773	Aai44773 Probe #13
32	1456	11.1	853	4	ABA31729	Aba31729 Probe #10
33	1456	11.1	853	4	ABA40773	Aba40773 Probe #19
34	1456	11.1	853	4	AAK50883	Aak50883 Human bon
35	1456	11.1	853	6	ABS12849	Abs12849 Human gen
36	1456	11.1	853	12	ACH91613	Ach91613 Human gen
37	1394	10.6	4048	8	ABZ74530	Abz74530 Secreted
38	1394	10.6	4048	10	ADC20955	Adc20955 Human sec
39	1394	10.6	4048	10	ABZ68064	Abz68064 Human sec
40	1390	10.6	1070	4	AAF23905	Aaf23905 Human sec
41	1390	10.6	1070	8	ABZ73615	Abz73615 Secreted
42	1390	10.6	1070	10	ADC20271	Adc20271 Human sec
43	1390	10.6	1070	10	ABZ67209	Abz67209 Human sec
c 44	1385	10.6	1065	4	AAF23936	Aaf23936 Human sec
c 45	1385	10.6	1065	8	ABZ73676	Abz73676 Secreted

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2006, 06:19:20 ; Search time 28880 Seconds
                                              (without alignments)
                                              8529.275 Million cell updates/sec

Title: US-10-723-361-3
Perfect score: 13101
Sequence: 1 MAISSRLALWEQKIREEDKS..........PGTGRKDDDVASIMKKYLQK 2568

Scoring table: BLOSUM62
                   Xgapop 10.0 , Xgapext   0.5
                   Ygapop 10.0 , Ygapext   0.5
                   Fgapop 6.0 , Fgapext   7.0
                   Delop   6.0 , Delext   7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10723361/runat_26062006_061903_27749/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10723361_@CGN_1_1_8328_@runat_26062006_061903_27749 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
                   1: gb_env:*
                   2: gb_pat:*
                   3: gb_ph:*
                   4: gb_pl:*
                   5: gb_pr:*
                   6: gb_ro:*
                   7: gb_sts:*
                   8: gb_sy:*
                   9: gb_un:*
                   10: gb_vi:*
                   11: gb_ov:*
                   12: gb_htg:*
                   13: gb_in:*
                   14: gb_om:*
                   15: gb_ba:*

          Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13101	100.0	7707	2	CQ615262	CQ615262 Sequence
	2	13101	100.0	7707	2	AR456326	AR456326 Sequence
	3	13101	100.0	8117	2	CQ615261	CQ615261 Sequence
	4	13101	100.0	8117	2	AR456325	AR456325 Sequence
	5	13101	100.0	8117	2	AX305149	AX305149 Sequence
	6	13101	100.0	8117	5	AY077700	AY077700 Homo sapi
	7	13059.5	99.7	8051	5	AB075376	AB075376 Homo sapi
	8	13041.5	99.5	8565	5	HSA310931	AJ310931 Homo sapi
	9	10438	79.7	6363	5	AB042648	AB042648 Homo sapi
	10	7911	60.4	4916	2	CQ615265	CQ615265 Sequence
	11	7911	60.4	4916	2	AR456328	AR456328 Sequence
	12	7262	55.4	4433	2	CQ729692	CQ729692 Sequence
	13	4799	36.6	2953	2	CQ615264	CQ615264 Sequence
	14	4799	36.6	2953	2	AR456327	AR456327 Sequence
	15	3717.5	28.4	7597	5	D86970	D86970 Homo sapien
	16	3707	28.3	7393	5	AB177858	AB177858 Homo sapi
	17	3647	27.8	7318	6	AB026497	AB026497 Mus muscu
	18	3645	27.8	6479	5	AB177860	AB177860 Homo sapi
	19	3645	27.8	6479	5	AY703984	AY703984 Homo sapi
	20	3640.5	27.8	6524	2	AX717783	AX717783 Sequence
	21	3580.5	27.3	7537	5	BC039612	BC039612 Homo sapi
	22	3542	27.0	6120	2	CQ724054	CQ724054 Sequence
	23	2562.5	19.6	1768	5	AK123936	AK123936 Homo sapi
	24	2561	19.5	1736	2	CS167736	CS167736 Sequence
	25	2561	19.5	1736	2	AX833857	AX833857 Sequence
	26	2561	19.5	1736	5	AK095943	AK095943 Homo sapi
	27	2375.5	18.1	288888	5	HSA310932	AJ310932 Homo sapi
c	28	2349	17.9	298575	12	HSBA22B4	AL080244 Homo sapi
c	29	2324.5	17.7	175756	12	AC148076	AC148076 Pan trogl
	30	2303	17.6	221507	5	HS407F11	AL022329 Human DNA
	31	2294	17.5	1314	2	CQ630927	CQ630927 Sequence
	32	2294	17.5	1314	2	AR471990	AR471990 Sequence
	33	2212	16.9	6223	13	AY051503	AY051503 Drosophil
	34	2143.5	16.4	4941	2	CQ598137	CQ598137 Sequence
	35	2113.5	16.1	5121	2	CQ613065	CQ613065 Sequence
	36	2100	16.0	1465	2	CQ142796	CQ142796 Sequence
	37	2100	16.0	1465	2	CQ178289	CQ178289 Sequence
	38	2100	16.0	73844	5	HSBK109D1	AL079300 Human DNA
	39	2095	16.0	1246	2	CQ630966	CQ630966 Sequence
	40	2095	16.0	1246	2	AR472029	AR472029 Sequence
	41	2084	15.9	4190	6	BC046638	BC046638 Mus muscu
	42	1456	11.1	853	2	CQ104600	CQ104600 Sequence
	43	1456	11.1	853	2	CQ155418	CQ155418 Sequence
	44	1456	11.1	853	2	CQ178799	CQ178799 Sequence
	45	1456	11.1	853	2	CQ187843	CQ187843 Sequence

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OM protein - protein search, using sw model

Run on: June 26, 2006, 08:28:12 ; Search time 28 Seconds
                                                (without alignments)
                                                2095.263 Million cell updates/sec

Title: US-10-723-361-3
Perfect score: 13101
Sequence: 1 MAISSRLALWEQKIREEDKS....`......PGTGRKDDDVASIMKKYLQK 2568

Scoring table: BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_New:*
                    1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                    2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                    3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                    4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                    5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                    6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                    7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                    8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2327	17.8	457	7	US-11-293-697-3424	Sequence 3424, Ap
2	657	5.0	2215	6	US-10-505-928-310	Sequence 310, App
3	610	4.7	1008	6	US-10-449-902-46459	Sequence 46459, A
4	571	4.4	923	6	US-10-449-902-54978	Sequence 54978, A
5	532	4.1	783	6	US-10-449-902-47723	Sequence 47723, A
6	484	3.7	3113	6	US-10-505-928-325	Sequence 325, App
7	449	3.4	2871	6	US-10-505-928-100	Sequence 100, App
8	447.5	3.4	863	7	US-11-293-697-3299	Sequence 3299, Ap
9	379.5	2.9	1328	6	US-10-504-973-32	Sequence 32, Appl
10	356.5	2.7	972	6	US-10-480-962-4	Sequence 4, Appli
11	345.5	2.6	1056	6	US-10-449-902-45516	Sequence 45516, A
12	337	2.6	726	7	US-11-334-351-2	Sequence 2, Appli
13	325	2.5	950	7	US-11-293-697-4492	Sequence 4492, Ap
14	321.5	2.5	2364	7	US-11-289-102-242	Sequence 242, App

15	311.5	2.4	3256	6	US-10-505-928-357	Sequence 357, App
16	304.5	2.3	531	6	US-10-953-349-20042	Sequence 20042, A
17	304.5	2.3	561	6	US-10-953-349-20041	Sequence 20041, A
18	304	2.3	2478	6	US-10-471-571A-2278	Sequence 2278, Ap
19	303.5	2.3	795	6	US-10-449-902-44893	Sequence 44893, A
20	302	2.3	696	6	US-10-449-902-28930	Sequence 28930, A
21	301	2.3	621	7	US-11-293-697-4409	Sequence 4409, Ap
22	296.5	2.3	980	7	US-11-289-102-296	Sequence 296, App
23	295.5	2.3	763	6	US-10-449-902-45594	Sequence 45594, A
24	293.5	2.2	694	6	US-10-449-902-37380	Sequence 37380, A
25	291.5	2.2	1032	6	US-10-449-902-45139	Sequence 45139, A
26	291	2.2	1309	6	US-10-449-902-41054	Sequence 41054, A
27	288	2.2	844	6	US-10-449-902-56744	Sequence 56744, A
28	287.5	2.2	901	6	US-10-449-902-51640	Sequence 51640, A
29	287	2.2	519	7	US-11-293-697-4747	Sequence 4747, Ap
30	286.5	2.2	824	7	US-11-293-697-3569	Sequence 3569, Ap
31	286	2.2	9535	6	US-10-471-571A-4496	Sequence 4496, Ap
32	285.5	2.2	1919	6	US-10-559-415-2	Sequence 2, Appli
33	283.5	2.2	1087	6	US-10-486-020-15	Sequence 15, Appl
34	279	2.1	990	7	US-11-293-697-3896	Sequence 3896, Ap
35	274	2.1	788	7	US-11-293-697-4150	Sequence 4150, Ap
36	270.5	2.1	1205	7	US-11-293-697-2967	Sequence 2967, Ap
37	270	2.1	1067	6	US-10-449-902-41164	Sequence 41164, A
38	269.5	2.1	1809	6	US-10-559-415-190	Sequence 190, App
39	268.5	2.0	1003	6	US-10-471-571A-4826	Sequence 4826, Ap
40	267	2.0	647	6	US-10-449-902-48454	Sequence 48454, A
41	266.5	2.0	602	6	US-10-953-349-11129	Sequence 11129, A
42	266.5	2.0	644	6	US-10-953-349-11128	Sequence 11128, A
43	266	2.0	1234	7	US-11-327-900-6	Sequence 6, Appli
44	261	2.0	624	6	US-10-449-902-54079	Sequence 54079, A
45	261	2.0	2186	6	US-10-471-571A-860	Sequence 860, App

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OM protein - protein search, using sw model

Run on: June 26, 2006, 08:26:52 ; Search time 286 Seconds
                                            (without alignments)
                                            4159.216 Million cell updates/sec

Title: US-10-723-361-3
Perfect score: 13101
Sequence: 1 MAISSRLALWEQKIREEDKS..........PGTGRKDDDVASIMKKYLQK 2568

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13101	100.0	2568	3	US-09-866-108-3	Sequence 3, Appli
2	13101	100.0	2568	4	US-10-723-361-3	Sequence 3, Appli
3	13031	99.5	2566	4	US-10-080-334-162	Sequence 162, App
4	13028	99.4	2566	4	US-10-080-334-163	Sequence 163, App
5	3666	28.0	2039	4	US-10-473-574-18	Sequence 18, Appl
6	3600.5	27.5	2035	4	US-10-080-334-160	Sequence 160, App
7	3572	27.3	1695	4	US-10-723-361-15753	Sequence 15753, A
8	3322	25.4	1581	4	US-10-080-334-159	Sequence 159, App
9	3322	25.4	1581	4	US-10-723-361-15754	Sequence 15754, A
10	3317.5	25.3	1596	4	US-10-080-334-42	Sequence 42, Appl
11	2892	22.1	1355	4	US-10-080-334-161	Sequence 161, App
12	2327	17.8	457	4	US-10-108-260A-3424	Sequence 3424, Ap
13	2135	16.3	1646	6	US-11-097-143-25896	Sequence 25896, A
14	2105	16.1	1706	6	US-11-097-143-40824	Sequence 40824, A
15	1620	12.4	311	4	US-10-029-386-33884	Sequence 33884, A
16	1302.5	9.9	1938	4	US-10-171-311-164	Sequence 164, App

17	1302.5	9.9	1938	5	US-10-995-561-661	Sequence 661, App
18	1302.5	9.9	1938	5	US-10-995-561-662	Sequence 662, App
19	1302.5	9.9	1954	5	US-10-995-561-660	Sequence 660, App
20	1302.5	9.9	1972	4	US-10-171-311-162	Sequence 162, App
21	1302.5	9.9	1972	4	US-10-341-434-103	Sequence 103, App
22	1302.5	9.9	1972	5	US-10-923-035-51	Sequence 51, Appl
23	1302.5	9.9	1972	5	US-10-995-561-664	Sequence 664, App
24	1302.5	9.9	1972	5	US-10-995-561-666	Sequence 666, App
25	1296	9.9	1945	3	US-09-927-597-2	Sequence 2, Appli
26	1296	9.9	1945	5	US-10-486-057-2	Sequence 2, Appli
27	1296	9.9	1979	3	US-09-927-597-4	Sequence 4, Appli
28	1296	9.9	1979	5	US-10-486-057-4	Sequence 4, Appli
29	1285.5	9.8	1976	6	US-11-069-834-54	Sequence 54, Appl
30	1280.5	9.8	1976	6	US-11-069-834-52	Sequence 52, Appl
31	1273	9.7	1961	4	US-10-028-248A-103	Sequence 103, App
32	1273	9.7	1961	4	US-10-107-782-103	Sequence 103, App
33	1268	9.7	1999	4	US-10-028-248A-107	Sequence 107, App
34	1268	9.7	1999	4	US-10-107-782-107	Sequence 107, App
35	1256	9.6	1959	4	US-10-028-248A-36	Sequence 36, Appl
36	1256	9.6	1959	4	US-10-107-782-36	Sequence 36, Appl
37	1247.5	9.5	1960	4	US-10-236-031B-62	Sequence 62, Appl
38	1247.5	9.5	1960	4	US-10-028-248A-104	Sequence 104, App
39	1247.5	9.5	1960	4	US-10-107-782-104	Sequence 104, App
40	1247.5	9.5	1960	5	US-10-696-909A-49	Sequence 49, Appl
41	1247.5	9.5	1960	5	US-10-530-171-17	Sequence 17, Appl
42	1247.5	9.5	1960	6	US-11-009-554-27	Sequence 27, Appl
43	1247.5	9.5	1960	6	US-11-069-834-50	Sequence 50, Appl
44	1240	9.5	2056	6	US-11-097-143-4824	Sequence 4824, Ap
45	1224	9.3	1960	5	US-10-805-684-90	Sequence 90, Appl

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OM protein - protein search, using sw model

Run on: June 26, 2006, 08:25:42 ; Search time 74 Seconds
                                           (without alignments)
                                           3037.549 Million cell updates/sec

Title: US-10-723-361-3
Perfect score: 13101
Sequence: 1 MAISSRLALWEQKIREEDKS..........PGTGRKDDDVASIMKKYLQK 2568

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
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                 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                 SUMMARIES

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1	13101	100.0	2568	2	US-09-866-108A-3	Sequence 3, Appli
2	3572	27.3	1695	2	US-09-866-108A-15753	Sequence 15753, A
3	3322	25.4	1581	2	US-09-866-108A-15754	Sequence 15754, A
4	1320	10.1	1972	2	US-08-875-435B-4	Sequence 4, Appli
5	1319	10.1	1972	2	US-08-875-435B-3	Sequence 3, Appli
6	1307.5	10.0	1984	2	US-09-949-016-7111	Sequence 7111, Ap
7	1307.5	10.0	1984	2	US-09-949-016-7112	Sequence 7112, Ap
8	1307.5	10.0	1984	2	US-09-949-016-7113	Sequence 7113, Ap
9	1302.5	9.9	1972	2	US-09-538-092-1084	Sequence 1084, Ap
10	1296	9.9	1945	2	US-09-927-597-2	Sequence 2, Appli
11	1296	9.9	1979	2	US-09-927-597-4	Sequence 4, Appli
12	1280.5	9.8	1976	2	US-09-538-092-1078	Sequence 1078, Ap
13	1248.5	9.5	1960	2	US-09-949-016-10872	Sequence 10872, A
14	1247.5	9.5	1960	2	US-09-538-092-1077	Sequence 1077, Ap
15	1181.5	9.0	1937	2	US-09-538-092-918	Sequence 918, App

16	1176	9.0	1857	2	US-09-917-254-91	Sequence 91, Appl
17	1173	9.0	1944	2	US-09-949-016-10929	Sequence 10929, A
18	1170	8.9	1935	2	US-09-538-092-916	Sequence 916, App
19	1169	8.9	1939	2	US-09-949-016-6925	Sequence 6925, Ap
20	1160	8.9	1942	2	US-09-949-016-8135	Sequence 8135, Ap
21	1158	8.8	1939	2	US-09-310-187A-1	Sequence 1, Appli
22	1158	8.8	1940	2	US-09-538-092-901	Sequence 901, App
23	1156.5	8.8	1939	2	US-09-538-092-917	Sequence 917, App
24	1156	8.8	1963	2	US-09-949-016-8888	Sequence 8888, Ap
25	1151.5	8.8	1939	2	US-09-538-092-915	Sequence 915, App
26	1151.5	8.8	1939	2	US-09-949-016-11104	Sequence 11104, A
27	1140	8.7	1938	2	US-09-949-016-6417	Sequence 6417, Ap
28	1135	8.7	1959	2	US-09-949-016-8134	Sequence 8134, Ap
29	1051	8.0	1886	2	US-08-938-105-3	Sequence 3, Appli
30	887.5	6.8	1120	2	US-09-147-404-1	Sequence 1, Appli
31	837.5	6.4	845	2	US-09-927-597-14	Sequence 14, Appl
32	831	6.3	852	2	US-09-927-597-12	Sequence 12, Appl
33	816	6.2	849	2	US-09-927-597-10	Sequence 10, Appl
34	799	6.1	1542	2	US-09-949-016-9215	Sequence 9215, Ap
35	664	5.1	2058	2	US-09-949-016-6835	Sequence 6835, Ap
36	654	5.0	2111	2	US-09-949-016-10199	Sequence 10199, A
37	648	4.9	772	2	US-09-927-597-8	Sequence 8, Appli
38	616	4.7	412	2	US-09-270-767-41984	Sequence 41984, A
39	607	4.6	864	2	US-09-248-796A-20612	Sequence 20612, A
40	605	4.6	2548	2	US-09-172-422-1	Sequence 1, Appli
41	598.5	4.6	699	2	US-09-927-597-6	Sequence 6, Appli
42	578	4.4	1236	2	US-09-883-134-4	Sequence 4, Appli
43	578	4.4	1236	2	US-10-306-879-4	Sequence 4, Appli
44	568.5	4.3	1113	2	US-10-094-749-2206	Sequence 2206, Ap
45	563.5	4.3	1285	2	US-09-976-594-507	Sequence 507, App

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          GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:           June 26, 2006, 08:33:37 ; Search time 462 Seconds
                                              (without alignments)
                                              5141.645 Million cell updates/sec

Title:            US-10-723-361-3
Perfect score:    2568
Sequence:         1 MAISSRLALWEQKIREEDKS..........PGTGRKDDDVASIMKKYLQK 2568


Scoring table:    OLIGO
                  Gapop 60.0 , Gapext 60.0

Searched:         2849598 seqs, 925015592 residues

Word size :       1

Total number of hits satisfying chosen parameters:        2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 250 summaries

Database :        UniProt_7.2:*
                  1:  uniprot_sprot:*
                  2:  uniprot_trembl:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.


                             SUMMARIES
                     %
Result             Query
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     2     1821    70.9   2566  2   Q5TF64_HUMAN          Q5tf64 homo sapien
     3      457    17.8    457  2   Q8N903_HUMAN          Q8n903 homo sapien
     4      291    11.3    668  2   Q68D67_HUMAN          Q68d67 homo sapien
     5       43     1.7    242  2   Q8C3H0_MOUSE          Q8c3h0 mus musculu
     6       43     1.7    745  2   Q9D4I1_MOUSE          Q9d4i1 mus musculu
     7       16     0.6   1972  2   Q4S1U4_TETNG          Q4s1u4 tetraodon n
     8       14     0.5    316  2   Q4TDQ8_TETNG          Q4tdq8 tetraodon n
     9       13     0.5    831  2   Q4S8N3_TETNG          Q4s8n3 tetraodon n
    10       12     0.5   1581  2   Q5QD01_HUMAN          Q5qd01 homo sapien
    11       12     0.5   1715  2   Q5W9F9_HUMAN          Q5w9f9 homo sapien
    12       12     0.5   2039  2   Q5H9U3_HUMAN          Q5h9u3 homo sapien
    13       12     0.5   2046  2   Q5W9G1_HUMAN          Q5w9g1 homo sapien
    14       12     0.5   2054  1   MY18A_HUMAN           Q92614 homo sapien
    15       10     0.4    201  2   O86010_SPHAR          O86010 sphingomona
    16       10     0.4    201  2   Q37ST5_SPHAR          Q37st5 novosphingo
    17       10     0.4    254  2   Q74EN7_GEOSL          Q74en7 geobacter s
    18       10     0.4    310  2   Q6CXM4_KLULA          Q6cxm4 kluyveromyc
    19       10     0.4    319  2   Q82HH3_STRAW          Q82hh3 streptomyce
    20       10     0.4    565  2   Q54M94_DICDI          Q54m94 dictyosteli
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21	10	0.4	596	2	Q5NBU1_ORYSA	Q5nbu1 oryza sativ
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23	10	0.4	1858	2	Q5TVZ3_ANOGA	Q5tvz3 anopheles g
24	10	0.4	1909	2	Q7QHD4_ANOGA	Q7qhd4 anopheles g
25	10	0.4	2754	2	Q4T1L1_TETNG	Q4t1l1 tetraodon n
26	9	0.4	112	2	Q5M7N5_XENTR	Q5m7n5 xenopus tro
27	9	0.4	116	2	O65276_ARATH	O65276 arabidopsis
28	9	0.4	123	2	Q6IDB4_ARATH	Q6idb4 arabidopsis
29	9	0.4	130	2	Q2QPV3_ORYSA	Q2qpv3 oryza sativ
30	9	0.4	139	2	Q5NBC7_ORYSA	Q5nbc7 oryza sativ
31	9	0.4	149	2	Q2WN45_CLOBE	Q2wn45 clostridium
32	9	0.4	160	2	Q2QNU2_ORYSA	Q2qnu2 oryza sativ
33	9	0.4	168	2	Q13108_HUMAN	Q13108 homo sapien
34	9	0.4	180	2	Q5CPX9_CRYPV	Q5cpx9 cryptospori
35	9	0.4	182	2	Q5CFD5_CRYHO	Q5cfd5 cryptospori
36	9	0.4	184	2	Q6AB20_PROAC	Q6ab20 propionibac
37	9	0.4	191	2	Q47NL2_THEFY	Q47nl2 thermobifid
38	9	0.4	198	2	Q6IJ63_DROME	Q6ij63 drosophila
39	9	0.4	199	2	Q8I6P8_ANOST	Q8i6p8 anopheles s
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41	9	0.4	226	2	P74140_SYNY3	P74140 synechocyst
42	9	0.4	229	2	Q46FM2_METBA	Q46fm2 methanosarc
43	9	0.4	233	2	Q3ISC1_NATPD	Q3isc1 natronomona
44	9	0.4	233	2	Q6AK44_DESPS	Q6ak44 desulfotale
45	9	0.4	250	2	Q60UV6_CAEBR	Q60uv6 caenorhabdi
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50	9	0.4	346	2	Q67M80_SYMTH	Q67m80 symbiobacte
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53	9	0.4	390	2	Q40VR2_KINRA	Q40vr2 kineococcus
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56	9	0.4	474	2	Q9AL96_9ACTO	Q9al96 streptomyce
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59	9	0.4	529	2	Q4UMI6_RICFE	Q4umi6 rickettsia
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61	9	0.4	535	2	Q6BVC6_DEBHA	Q6bvc6 debaryomyce
62	9	0.4	538	2	Q41LZ5_METBU	Q41lz5 methanococc
63	9	0.4	547	2	Q6NKK4_CORDI	Q6nkk4 corynebacte
64	9	0.4	568	2	Q98JH0_RHILO	Q98jh0 rhizobium l
65	9	0.4	573	2	Q74DV0_GEOSL	Q74dv0 geobacter s
66	9	0.4	574	2	Q4CBE4_CLOTM	Q4cbe4 clostridium
67	9	0.4	575	2	Q811J9_MOUSE	Q811j9 mus musculu
68	9	0.4	597	2	Q92V59_RHIME	Q92v59 rhizobium m
69	9	0.4	616	2	Q8UD85_AGRT5	Q8ud85 agrobacteri
70	9	0.4	617	2	Q92PE4_RHIME	Q92pe4 rhizobium m
71	9	0.4	618	2	Q2K5S7_RHIET	Q2k5s7 rhizobium e
72	9	0.4	624	2	Q3QY46_9RHOB	Q3qy46 silicibacte
73	9	0.4	625	2	O02717_BOVIN	O02717 bos taurus
74	9	0.4	633	2	Q7CXJ3_AGRT5	Q7cxj3 agrobacteri
75	9	0.4	639	1	Y1819_MYCTU	Q50614 mycobacteri
76	9	0.4	639	2	Q73ZS0_MYCPA	Q73zs0 mycobacteri
77	9	0.4	639	2	Q7TZG9_MYCBO	Q7tzg9 mycobacteri
78	9	0.4	663	2	Q7ULL7_RHOBA	Q7ull7 rhodopirell
79	9	0.4	682	2	Q4NLR2_9MICC	Q4nlr2 arthrobacte
80	9	0.4	711	2	Q2TAK8_HUMAN	Q2tak8 homo sapien
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85	9	0.4	790	2	Q7S0W4_NEUCR	Q7s0w4 neurospora
86	9	0.4	791	2	Q6ZK51_ORYSA	Q6zk51 oryza sativ
87	9	0.4	835	2	Q9SDN5_TOBAC	Q9sdn5 nicotiana t
88	9	0.4	837	2	Q6PB65_MOUSE	Q6pb65 mus musculu
89	9	0.4	873	2	Q3UV60_MOUSE	Q3uv60 mus musculu
90	9	0.4	895	2	Q811I2_MOUSE	Q811i2 mus musculu
91	9	0.4	953	2	Q7RDI4_PLAYO	Q7rdi4 plasmodium
92	9	0.4	959	2	Q3UFT0_MOUSE	Q3uft0 mus musculu
93	9	0.4	1081	2	Q57ZX4_9TRYP	Q57zx4 trypanosoma
94	9	0.4	1085	2	Q4ING2_GIBZE	Q4ing2 gibberella
95	9	0.4	1158	2	Q4KMN4_MOUSE	Q4kmn4 mus musculu
96	9	0.4	1227	2	Q9LXF4_ARATH	Q9lxf4 arabidopsis
97	9	0.4	1327	1	MYH11_RAT	Q63862 rattus norv
98	9	0.4	1331	2	Q86T83_HUMAN	Q86t83 homo sapien
99	9	0.4	1335	2	Q6KAN6_MOUSE	Q6kan6 mus musculu
100	9	0.4	1398	2	Q4S0W3_TETNG	Q4s0w3 tetraodon n
101	9	0.4	1477	2	Q4T443_TETNG	Q4t443 tetraodon n
102	9	0.4	1700	2	Q3TBB2_MOUSE	Q3tbb2 mus musculu
103	9	0.4	1719	2	Q4QD97_LEIMA	Q4qd97 leishmania
104	9	0.4	1722	2	Q3UH48_MOUSE	Q3uh48 mus musculu
105	9	0.4	1833	2	Q80T68_MOUSE	Q80t68 mus musculu
106	9	0.4	1907	2	Q5ICW5_BRARE	Q5icw5 brachydanio
107	9	0.4	1938	2	Q5SWW5_MOUSE	Q5sww5 mus musculu
108	9	0.4	1959	1	MYH9_CHICK	P14105 gallus gall
109	9	0.4	1959	1	MYH9_HUMAN	P35579 homo sapien
110	9	0.4	1959	1	MYH9_MOUSE	Q8vdd5 mus musculu
111	9	0.4	1960	1	MYH9_RAT	Q62812 rattus norv
112	9	0.4	1960	2	Q60FE2_HUMAN	Q60fe2 homo sapien
113	9	0.4	1960	2	Q3UHU4_MOUSE	Q3uhu4 m 15 days p
114	9	0.4	1964	2	O93522_XENLA	O93522 xenopus lae
115	9	0.4	1972	1	MYH11_MOUSE	O08638 mus musculu
116	9	0.4	1972	1	MYH11_RABIT	P35748 oryctolagus
117	9	0.4	1972	2	Q8R384_MOUSE	Q8r384 mus musculu
118	9	0.4	1974	2	Q4U0S2_BRARE	Q4u0s2 brachydanio
119	9	0.4	1976	1	MYH10_BOVIN	Q27991 bos taurus
120	9	0.4	1976	1	MYH10_HUMAN	P35580 homo sapien
121	9	0.4	1976	1	MYH10_MOUSE	Q61879 mus musculu
122	9	0.4	1976	1	MYH10_RAT	Q9jlt0 rattus norv
123	9	0.4	1976	2	Q789A6_CHICK	Q789a6 gallus gall
124	9	0.4	1978	1	MYH11_CHICK	P10587 gallus gall
125	9	0.4	1984	2	Q69ZX3_MOUSE	Q69zx3 mus musculu
126	9	0.4	1986	2	Q789A5_CHICK	Q789a5 gallus gall
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128	9	0.4	1997	2	Q02015_CHICK	Q02015 gallus gall
129	9	0.4	1998	2	Q5SYP1_MOUSE	Q5syp1 mus musculu
130	9	0.4	1999	2	Q63731_RAT	Q63731 rattus norv
131	9	0.4	2007	2	Q5SV64_MOUSE	Q5sv64 mus musculu
132	9	0.4	2007	2	Q789A4_CHICK	Q789a4 gallus gall
133	9	0.4	2013	2	Q3UH59_MOUSE	Q3uh59 mus musculu
134	9	0.4	2018	2	Q4LE45_HUMAN	Q4le45 homo sapien
135	9	0.4	2031	2	Q3UHT9_MOUSE	Q3uht9 mus musculu
136	9	0.4	2035	1	MY18A_MOUSE	Q9jmh9 mus musculu
137	9	0.4	2035	2	Q5SYP0_MOUSE	Q5syp0 mus musculu
138	9	0.4	2046	2	Q4SAT5_TETNG	Q4sat5 tetraodon n
139	9	0.4	2050	2	Q5SYN9_MOUSE	Q5syn9 mus musculu
140	9	0.4	2110	2	Q54BP1_DICDI	Q54bp1 dictyosteli
141	9	0.4	2124	2	Q4RLE9_TETNG	Q4rle9 tetraodon n
142	9	0.4	2310	2	Q4T4L3_TETNG	Q4t4l3 tetraodon n

143	9	0.4	2332	2	Q4A2B5_9PHYC	Q4a2b5	emiliania h
144	8	0.3	36	2	Q7TMZ1_MOUSE	Q7tmz1	mus musculu
145	8	0.3	43	2	Q5K0A1_9FUNG	Q5k0a1	orpinomyces
146	8	0.3	48	2	O04217_BROFI	O04217	bromheadia
147	8	0.3	54	2	Q5XI92_RAT	Q5xi92	rattus norv
148	8	0.3	66	2	Q9WML9_9ENTO	Q9wml9	human polio
149	8	0.3	73	2	O62023_CAEEL	O62023	caenorhabdi
150	8	0.3	73	2	Q60QL4_CAEBR	Q60ql4	caenorhabdi
151	8	0.3	74	2	Q5S1X9_IXOSC	Q5s1x9	ixodes scap
152	8	0.3	75	2	Q4KLT7_XENLA	Q4klt7	xenopus lae
153	8	0.3	75	2	Q6GM97_XENLA	Q6gm97	xenopus lae
154	8	0.3	76	1	ZN706_CHICK	Q5zmm5	gallus gall
155	8	0.3	76	1	ZN706_HUMAN	Q9y5v0	homo sapien
156	8	0.3	76	1	ZN706_MOUSE	Q9d115	mus musculu
157	8	0.3	76	2	Q9HB72_HUMAN	Q9hb72	homo sapien
158	8	0.3	76	2	Q32P60_BOVIN	Q32p60	bos taurus
159	8	0.3	76	2	Q4SSG5_TETNG	Q4ssg5	tetraodon n
160	8	0.3	76	2	Q6AZC6_BRARE	Q6azc6	brachydanio
161	8	0.3	78	2	Q4JTE3_CORJK	Q4jte3	corynebacte
162	8	0.3	84	2	Q38Y32_LACSS	Q38y32	lactobacill
163	8	0.3	85	2	Q8JLY9_9NUCL	Q8jly9	mamestra co
164	8	0.3	87	2	Q97GJ4_CLOAB	Q97gj4	clostridium
165	8	0.3	88	2	Q8PJM5_XANAC	Q8pjm5	xanthomonas
166	8	0.3	89	2	Q884I0_PSESM	Q884i0	pseudomonas
167	8	0.3	94	2	Q3E7K6_ARATH	Q3e7k6	arabidopsis
168	8	0.3	95	2	Q3FYQ3_9DELT	Q3fyq3	pelobacter
169	8	0.3	99	2	Q4RI45_TETNG	Q4ri45	tetraodon n
170	8	0.3	99	2	Q4SFJ8_TETNG	Q4sfj8	tetraodon n
171	8	0.3	103	2	Q2LZ98_DROPS	Q2lz98	drosophila
172	8	0.3	103	2	Q6J5F5_HAEIN	Q6j5f5	haemophilus
173	8	0.3	106	2	Q40NN6_DESAC	Q40nn6	desulfuromo
174	8	0.3	112	2	Q9YBD3_AERPE	Q9ybd3	aeropyrum p
175	8	0.3	118	2	Q2J820_9ACTO	Q2j820	frankia sp.
176	8	0.3	118	2	Q80HS7_WSSV	Q80hs7	white spot
177	8	0.3	122	2	Q63298_RAT	Q63298	rattus norv
178	8	0.3	123	2	Q3FEK0_9BURK	Q3fek0	burkholderi
179	8	0.3	125	2	Q6ZFV0_ORYSA	Q6zfv0	oryza sativ
180	8	0.3	126	2	Q96W44_OPHNO	Q96w44	ophiostoma
181	8	0.3	128	2	O35133_9MURI	O35133	rattus sp.
182	8	0.3	130	2	Q40VE0_KINRA	Q40ve0	kineococcus
183	8	0.3	132	2	Q2S639_9SPHI	Q2s639	salinibacte
184	8	0.3	136	2	Q7NZE7_CHRVO	Q7nze7	chromobacte
185	8	0.3	138	2	Q5TKP5_ORYSA	Q5tkp5	oryza sativ
186	8	0.3	140	2	Q5C5V7_SCHJA	Q5c5v7	schistosoma
187	8	0.3	140	2	Q4RXT2_TETNG	Q4rxt2	tetraodon n
188	8	0.3	141	2	Q6K5B9_ORYSA	Q6k5b9	oryza sativ
189	8	0.3	141	2	Q5NY95_AZOSE	Q5ny95	azoarcus sp
190	8	0.3	142	2	Q3CPP2_ALTAT	Q3cpp2	pseudoalter
191	8	0.3	143	2	Q6IHW9_DROME	Q6ihw9	drosophila
192	8	0.3	144	2	Q4BZI1_CROWT	Q4bzi1	crocosphaer
193	8	0.3	149	2	Q5DHA0_SCHJA	Q5dha0	schistosoma
194	8	0.3	150	2	Q4X606_PLACH	Q4x606	plasmodium
195	8	0.3	150	2	Q4YBI1_PLABE	Q4ybi1	plasmodium
196	8	0.3	150	2	Q7RNR3_PLAYO	Q7rnr3	plasmodium
197	8	0.3	150	2	Q68842_9HEPC	Q68842	hepatitis c
198	8	0.3	151	2	Q46AZ1_METBA	Q46az1	methanosarc
199	8	0.3	151	2	Q4CMW2_TRYCR	Q4cmw2	trypanosoma
200	8	0.3	151	2	Q6GZM1_MALRU	Q6gzm1	malonomonas
201	8	0.3	151	2	Q5P8G9_AZOSE	Q5p8g9	azoarcus sp
202	8	0.3	155	2	Q7WSZ7_9BACE	Q7wsz7	bacteroides
203	8	0.3	156	2	Q2UU94_ASPOR	Q2uu94	aspergillus

204	8	0.3	157	2	Q3H083_9ACTO	Q3h083	nocardioide
205	8	0.3	159	2	Q8GBL4_9BACT	Q8gbl4	uncultured
206	8	0.3	159	2	Q57AG7_BRUAB	Q57ag7	brucella ab
207	8	0.3	159	2	Q8FY02_BRUSU	Q8fy02	brucella su
208	8	0.3	159	2	Q8YE44_BRUME	Q8ye44	brucella me
209	8	0.3	159	2	Q2YQY2_BRUA2	Q2yqy2	brucella ab
210	8	0.3	162	2	Q3X3S9_9ACTN	Q3x3s9	rubrobacter
211	8	0.3	163	2	Q8GY17_ARATH	Q8gy17	arabidopsis
212	8	0.3	164	2	Q3SG72_THIDA	Q3sg72	thiobacillu
213	8	0.3	166	2	Q63297_RAT	Q63297	rattus norv
214	8	0.3	169	2	Q9Y4Y6_HUMAN	Q9y4y6	homo sapien
215	8	0.3	169	2	Q9ZW05_ARATH	Q9zw05	arabidopsis
216	8	0.3	172	2	Q5ZQX5_9CAUD	Q5zqx5	bacteriopha
217	8	0.3	172	2	Q402V1_9BACT	Q402v1	uncultured
218	8	0.3	172	2	Q402V8_9BACT	Q402v8	uncultured
219	8	0.3	172	2	Q52UW6_9BACT	Q52uw6	uncultured
220	8	0.3	173	2	Q4I357_GIBZE	Q4i357	gibberella
221	8	0.3	173	2	O08882_RAT	O08882	rattus norv
222	8	0.3	174	2	Q7PND0_ANOGA	Q7pnd0	anopheles g
223	8	0.3	175	2	Q6BC92_SCHMA	Q6bc92	schistosoma
224	8	0.3	182	2	Q5ZDX0_ORYSA	Q5zdx0	oryza sativ
225	8	0.3	184	2	Q8TA33_HETGL	Q8ta33	heterodera
226	8	0.3	186	2	Q9YHV6_FUGRU	Q9yhv6	fugu rubrip
227	8	0.3	187	2	Q33IT7_METHU	Q33it7	methanospir
228	8	0.3	187	2	Q4QEX7_LEIMA	Q4qex7	leishmania
229	8	0.3	188	2	Q32ND6_HUMAN	Q32nd6	homo sapien
230	8	0.3	192	2	Q3AJR3_SYNSC	Q3ajr3	synechococc
231	8	0.3	197	1	CFI2_MEDSA	P28013	medicago sa
232	8	0.3	198	2	Q4CN86_TRYCR	Q4cn86	trypanosoma
233	8	0.3	205	2	Q64GK6_STRCV	Q64gk6	streptococc
234	8	0.3	206	2	Q4NCA5_9MICC	Q4nca5	arthrobacte
235	8	0.3	208	2	Q9JZS9_NEIMB	Q9jzs9	neisseria m
236	8	0.3	208	2	Q9DG56_BRARE	Q9dg56	brachydanio
237	8	0.3	209	2	Q3K707_PSEPF	Q3k707	pseudomonas
238	8	0.3	209	2	Q4K6D4_PSEF5	Q4k6d4	pseudomonas
239	8	0.3	210	2	Q48MR3_PSE14	Q48mr3	pseudomonas
240	8	0.3	210	2	Q4ZXS7_PSEU2	Q4zxs7	pseudomonas
241	8	0.3	210	2	Q2JTW7_9CYAN	Q2jtw7	cyanobacter
242	8	0.3	210	2	Q887Y3_PSESM	Q887y3	pseudomonas
243	8	0.3	212	2	Q72E32_DESVH	Q72e32	desulfovibr
244	8	0.3	214	2	Q39763_GOSBA	Q39763	gossypium b
245	8	0.3	214	2	Q39789_GOSHI	Q39789	gossypium h
246	8	0.3	215	2	Q6LYE1_METMP	Q6lye1	methanococc
247	8	0.3	215	2	Q67V24_ORYSA	Q67v24	oryza sativ
248	8	0.3	215	2	Q6FB36_ACIAD	Q6fb36	acinetobact
249	8	0.3	219	1	VG11_BPT4	P10929	bacteriopha
250	8	0.3	219	2	Q8JU39_9CAUD	Q8ju39	phage arl.

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OM protein - protein search, using sw model

Run on:          June 26, 2006, 08:38:43 ; Search time 71 Seconds
                                           (without alignments)
                                           3480.065 Million cell updates/sec

Title:           US-10-723-361-3
Perfect score:   2568
Sequence:        1 MAISSRLALWEQKIREEDKS..........PGTGRKDDDVASIMKKYLQK 2568


Scoring table:   OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched:        283416 seqs, 96216763 residues

Word size :      1

Total number of hits satisfying chosen parameters:       283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 250 summaries

Database :       PIR_80:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                               SUMMARIES
                 %
Result         Query
  No.  Score  Match Length DB   ID                    Description
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     1    10    0.4    201  2   T31302                hypothetical prote
     2     9    0.4    116  2   T01231                hypothetical prote
     3     9    0.4    168  2   I38944                melanoma ubiquitou
     4     9    0.4    226  2   S75665                ABC-type transport
     5     9    0.4    248  2   S23449                NADH oxidase (H2O2
     6     9    0.4    292  2   H70313                cobalamin synthesi
     7     9    0.4    438  2   I38946                melanoma ubiquitou
     8     9    0.4    597  2   A95949                hypothetical prote
     9     9    0.4    616  2   AI2851                hypothetical prote
    10     9    0.4    621  2   S10450                myosin heavy chain
    11     9    0.4    633  2   G97628                ATP-binding protei
    12     9    0.4    639  2   D70720                hypothetical prote
    13     9    0.4    766  2   A86198                hypothetical prote
    14     9    0.4    790  2   T49542                xylan 1,4-beta-xyl
    15     9    0.4   1227  2   T49963                hypothetical prote
    16     9    0.4   1938  2   JC5421                smooth muscle myos
    17     9    0.4   1959  1   A33977                myosin heavy chain
    18     9    0.4   1961  1   A61231                myosin heavy chain
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19	9	0.4	1964	2	A59282	nonmuscle myosin I
20	9	0.4	1972	1	A41604	myosin heavy chain
21	9	0.4	1972	2	JC5420	smooth muscle myos
22	9	0.4	1976	2	A59252	myosin heavy chain
23	9	0.4	1979	1	S03166	myosin heavy chain
24	9	0.4	1992	2	A47297	myosin heavy chain
25	9	0.4	1999	1	S21801	myosin heavy chain
26	9	0.4	2007	1	B43402	myosin heavy chain
27	8	0.3	73	2	T18810	hypothetical prote
28	8	0.3	87	2	E97192	small acid-soluble
29	8	0.3	112	2	D72547	hypothetical prote
30	8	0.3	159	2	AD3506	sensor protein chv
31	8	0.3	169	2	D84693	hypothetical prote
32	8	0.3	208	2	B81142	hypothetical prote
33	8	0.3	214	2	T10737	extensin-like cell
34	8	0.3	214	2	T09854	proline-rich cell
35	8	0.3	219	1	GLBPT4	baseplate protein
36	8	0.3	222	2	S44371	chalcone isomerase
37	8	0.3	223	2	T06421	chalcone isomerase
38	8	0.3	240	2	A64360	hypothetical prote
39	8	0.3	243	2	C95908	hypothetical prote
40	8	0.3	244	2	A72551	hypothetical prote
41	8	0.3	273	2	D47301	VirB9 homolog - Bo
42	8	0.3	274	2	JQ2159	hypothetical 30.6K
43	8	0.3	274	2	JQ2145	movement protein -
44	8	0.3	280	2	T03543	probable cobalt tr
45	8	0.3	315	2	T06806	proline rich prote
46	8	0.3	328	2	H87535	hypothetical prote
47	8	0.3	329	2	H72421	hypothetical prote
48	8	0.3	341	2	AB0785	probable binding-p
49	8	0.3	341	2	A85857	probable transport
50	8	0.3	341	2	G91012	probable transport
51	8	0.3	341	2	B64987	hypothetical 38.1
52	8	0.3	351	2	S21345	retrovirus-related
53	8	0.3	364	2	T43467	hypothetical prote
54	8	0.3	365	2	A95042	UDP-N-acetylglucos
55	8	0.3	366	2	H82425	molybdenum ABC tra
56	8	0.3	379	2	A48936	nitrite reductase
57	8	0.3	383	2	A95964	probable 2-aminoet
58	8	0.3	391	2	H70041	probable transcrip
59	8	0.3	399	2	A75269	acetyl-CoA acetylt
60	8	0.3	412	2	S69633	hypothetical prote
61	8	0.3	424	2	B95964	probable phosphono
62	8	0.3	429	1	C64100	phosphoribosylamin
63	8	0.3	437	2	T14192	extensin homolog T
64	8	0.3	437	2	JC4929	transcription fact
65	8	0.3	460	2	H96536	hypothetical prote
66	8	0.3	482	2	S74982	cobyrinic acid a,c
67	8	0.3	521	2	E95052	hypothetical prote
68	8	0.3	530	2	B36921	methyl coenzyme M
69	8	0.3	555	2	T38108	high-affinity gluc
70	8	0.3	620	2	S06733	hydroxyproline-ric
71	8	0.3	627	2	T25395	hypothetical prote
72	8	0.3	634	2	T45941	pasticcino 1 - Ara
73	8	0.3	710	2	D96728	hypothetical prote
74	8	0.3	723	2	C83412	probable ATP-bindi
75	8	0.3	728	2	H59435	phosphoinositide-3
76	8	0.3	731	2	T04455	hypothetical prote
77	8	0.3	772	2	T02098	probable phosphati
78	8	0.3	779	2	T47756	phosphatidylinosit
79	8	0.3	808	2	T15562	hypothetical prote

80	8	0.3	953	2	S75285	methyl-accepting c
81	8	0.3	1135	2	T30561	Scythe protein - A
82	8	0.3	1225	2	A49464	chromosome segrega
83	8	0.3	1255	2	T31065	diaphanous protein
84	8	0.3	1389	2	I58157	periaxin - rat
85	8	0.3	1528	2	A60338	surface antigen A
86	8	0.3	1556	2	A60988	saliva-interacting
87	8	0.3	1561	1	S06839	surface antigen sp
88	8	0.3	1565	2	S04729	surface antigen pa
89	8	0.3	1566	2	A43607	cell surface antig
90	8	0.3	1630	2	T00390	KIAA0614 protein -
91	8	0.3	1838	1	CGHU1V	collagen alpha 1(V
92	8	0.3	1843	2	S18803	collagen alpha 1(V
93	8	0.3	2222	2	T13924	sdk protein - frui
94	8	0.3	2554	2	AB3528	extracellular seri
95	7	0.3	14	2	S29789	hypothetical prote
96	7	0.3	55	2	PQ0435	genome polyprotein
97	7	0.3	55	2	PQ0433	genome polyprotein
98	7	0.3	56	2	PQ0436	genome polyprotein
99	7	0.3	56	2	PQ0437	genome polyprotein
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101	7	0.3	56	2	PQ0432	genome polyprotein
102	7	0.3	56	2	PQ0429	genome polyprotein
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104	7	0.3	56	2	PQ0431	genome polyprotein
105	7	0.3	56	2	PQ0427	genome polyprotein
106	7	0.3	56	2	PQ0430	genome polyprotein
107	7	0.3	58	2	S29147	superoxide dismuta
108	7	0.3	58	2	F86103	hypothetical prote
109	7	0.3	60	2	S60851	M protein precurso
110	7	0.3	60	2	H97206	probable membrane
111	7	0.3	61	2	A64889	ynbE protein precu
112	7	0.3	63	1	IHQFT	high potential iro
113	7	0.3	63	1	H64095	carbon storage reg
114	7	0.3	73	2	AB2468	secretory protein
115	7	0.3	76	2	AE2700	conserved hypothet
116	7	0.3	81	2	F82731	hypothetical prote
117	7	0.3	82	2	S24629	H+-transporting tw
118	7	0.3	86	2	F90490	hypothetical prote
119	7	0.3	90	2	E97482	hypothetical 8.2K
120	7	0.3	100	2	S34400	NADH2 dehydrogenas
121	7	0.3	100	2	C44866	major merozoite su
122	7	0.3	100	2	T09148	late-embryogenesis
123	7	0.3	102	2	S69741	hypothetical prote
124	7	0.3	103	2	I58936	hypothetical prote
125	7	0.3	105	2	E69326	hypothetical prote
126	7	0.3	106	2	JC7778	hepatocyte growth
127	7	0.3	107	2	B85356	glycine-rich prote
128	7	0.3	110	2	C55228	hypothetical prote
129	7	0.3	111	2	F82219	PTS system, cellob
130	7	0.3	112	2	H64215	hypothetical prote
131	7	0.3	112	2	B35308	cAMP-regulated pho
132	7	0.3	113	2	T09515	hypothetical prote
133	7	0.3	115	2	S60397	hypothetical prote
134	7	0.3	115	2	T50390	hypothetical prote
135	7	0.3	115	2	T43354	nuclear receptor N
136	7	0.3	119	2	A23063	pancreatic B-cell
137	7	0.3	119	2	T13520	hypothetical prote
138	7	0.3	119	2	C89582	protein C18A11.1 [
139	7	0.3	124	2	T45917	hypothetical prote
140	7	0.3	125	2	T49356	hypothetical prote

141	7	0.3	127	2	A54670	RNA polymerase II
142	7	0.3	127	2	A28084	DNA-binding protei
143	7	0.3	129	2	S60974	hypothetical prote
144	7	0.3	129	2	T31200	hypothetical prote
145	7	0.3	129	2	AI2799	conserved hypothet
146	7	0.3	129	2	C97579	hesb family protei
147	7	0.3	130	2	S12308	TAS14 protein - to
148	7	0.3	131	2	A53024	Leydig insulin-lik
149	7	0.3	134	2	T46114	hypothetical prote
150	7	0.3	134	2	AG3208	hypothetical prote
151	7	0.3	135	2	C82176	hypothetical prote
152	7	0.3	137	2	T51202	hypothetical prote
153	7	0.3	138	2	I39641	toxin I - Actinoba
154	7	0.3	139	2	G98226	hypothetical prote
155	7	0.3	139	2	AI3059	hypothetical prote
156	7	0.3	140	2	A38845	flagellar protein
157	7	0.3	140	2	C72705	hypothetical prote
158	7	0.3	140	2	H71033	hypothetical prote
159	7	0.3	141	2	G83312	probable type II s
160	7	0.3	141	2	H64361	hypothetical prote
161	7	0.3	143	2	T29840	hypothetical prote
162	7	0.3	144	2	S51720	regulatory protein
163	7	0.3	146	2	F64000	hypothetical prote
164	7	0.3	146	2	S31638	hypothetical prote
165	7	0.3	149	1	E69073	NADP-reducing hydr
166	7	0.3	149	2	A46132	c-Jun leucine zipp
167	7	0.3	153	2	E81708	conserved hypothet
168	7	0.3	154	2	T04538	hypothetical prote
169	7	0.3	155	2	H69285	adenylylsulfate 3-
170	7	0.3	157	2	AC1190	ABC transporter, A
171	7	0.3	158	2	AB1893	hypothetical prote
172	7	0.3	159	2	T04173	heat shock protein
173	7	0.3	160	2	A75466	2-demethylmenaquin
174	7	0.3	160	2	E72631	hypothetical prote
175	7	0.3	162	2	A69543	hypothetical prote
176	7	0.3	163	2	T33933	hypothetical prote
177	7	0.3	164	2	G64132	phosphoribosylamin
178	7	0.3	164	2	H70444	hypothetical prote
179	7	0.3	165	2	F87661	hypothetical prote
180	7	0.3	165	2	F84102	flagellar protein
181	7	0.3	166	2	JC1348	hypothetical 18K p
182	7	0.3	166	2	S13219	s18 protein - frui
183	7	0.3	168	2	A70419	glycerol-3-phospha
184	7	0.3	168	2	T05173	hypothetical prote
185	7	0.3	172	2	F87675	MutT/nudix family
186	7	0.3	174	2	F75097	adenylylsulfate 3-
187	7	0.3	174	2	T51542	hypothetical prote
188	7	0.3	176	2	F72651	hypothetical prote
189	7	0.3	177	1	S74917	adenylyl-sulfate k
190	7	0.3	178	2	B82124	hypothetical prote
191	7	0.3	179	2	B84587	probable glutaredo
192	7	0.3	179	2	AB1974	hypothetical prote
193	7	0.3	179	2	T30460	hypothetical prote
194	7	0.3	185	2	F96789	protein T23E18.12
195	7	0.3	186	2	A89992	hypothetical prote
196	7	0.3	189	2	T30352	hypothetical prote
197	7	0.3	190	1	RHSHCE	corticoliberin pre
198	7	0.3	190	2	D72515	hypothetical prote
199	7	0.3	193	2	E86233	hypothetical prote
200	7	0.3	195	2	B75273	hypothetical prote
201	7	0.3	197	2	S53334	streptokinase - St

202	7	0.3	198	2	T49955	40S ribosomal prot
203	7	0.3	198	2	G82265	syd protein VC0903
204	7	0.3	199	2	A61513	myosin, sarcomeric
205	7	0.3	199	2	T14468	pollen coat protei
206	7	0.3	199	2	S16063	acp-22 protein - y
207	7	0.3	199	2	S32224	acp-22 protein - y
208	7	0.3	202	2	A71935	hypothetical prote
209	7	0.3	202	2	T11744	dehydrin - kidney
210	7	0.3	203	1	S50980	NHP10 protein - ye
211	7	0.3	204	2	AB3024	transcription regu
212	7	0.3	205	2	A81011	thiamin-phosphate
213	7	0.3	205	2	E82032	thiamine-phosphate
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218	7	0.3	205	2	S41002	hypothetical prote
219	7	0.3	206	2	H72649	hypothetical prote
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221	7	0.3	207	2	D84110	hypothetical prote
222	7	0.3	211	2	B71341	conserved hypothet
223	7	0.3	212	2	C75330	thymidine kinase (
224	7	0.3	213	2	AF2283	hypothetical prote
225	7	0.3	213	2	E71190	hypothetical prote
226	7	0.3	214	1	S18729	adenylyl-sulfate k
227	7	0.3	214	2	D59108	hypothetical prote
228	7	0.3	216	2	S50766	dehydrin-related p
229	7	0.3	217	2	H72350	hypothetical prote
230	7	0.3	218	2	C86337	hypothetical prote
231	7	0.3	218	2	T45979	hypothetical prote
232	7	0.3	219	2	AG2036	hypothetical prote
233	7	0.3	219	2	T06302	hypothetical prote
234	7	0.3	222	2	A75406	hydrolase - Deinoc
235	7	0.3	222	2	D86582	uridine kinase [im
236	7	0.3	222	2	E72041	uridine kinase CP0
237	7	0.3	222	2	A89776	capsular polysacch
238	7	0.3	222	2	B49599	polymerase-associa
239	7	0.3	222	2	AG1207	ABC transporter (A
240	7	0.3	226	2	A86268	hypothetical prote
241	7	0.3	226	2	T36096	probable secreted
242	7	0.3	227	2	C64424	hypothetical prote
243	7	0.3	229	2	E82682	GTP-binding protei
244	7	0.3	229	2	T48534	hypothetical prote
245	7	0.3	229	2	T52364	hypothetical prote
246	7	0.3	231	2	A95030	acetyltransferase,
247	7	0.3	231	2	S62530	hypothetical prote
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249	7	0.3	232	1	S31235	imidazoleglycerol-
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     GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:            June 26, 2006, 08:48:53 ; Search time 28 Seconds
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Scoring table:  OLIGO
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Searched:       99297 seqs, 22845552 residues

Word size :     1

Total number of hits satisfying chosen parameters:      99283

Minimum DB seq length: 0
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Post-processing: Listing first 250 summaries

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        Pred. No. is the number of results predicted by chance to have a
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        and is derived by analysis of the total score distribution.
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SUMMARIES

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3	9	0.4	210	6	US-10-953-349-23295	Sequence 23295, A
4	8	0.3	42	6	US-10-526-722-10	Sequence 10, Appl
5	8	0.3	42	6	US-10-526-722-52	Sequence 52, Appl
6	8	0.3	42	6	US-10-526-722-110	Sequence 110, App
7	8	0.3	97	6	US-10-953-349-37158	Sequence 37158, A
8	8	0.3	109	7	US-11-293-697-4725	Sequence 4725, Ap
9	8	0.3	126	6	US-10-449-902-49797	Sequence 49797, A
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13	8	0.3	342	6	US-10-953-349-16687	Sequence 16687, A
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226	7	0.3	150	2	US-09-599-360B-90	Sequence 90, Appl
227	7	0.3	150	2	US-09-513-999C-6317	Sequence 6317, Ap
228	7	0.3	151	2	US-08-946-329A-47	Sequence 47, Appl
229	7	0.3	151	2	US-09-562-914-47	Sequence 47, Appl
230	7	0.3	153	2	US-09-270-767-37175	Sequence 37175, A
231	7	0.3	153	2	US-09-270-767-52392	Sequence 52392, A
232	7	0.3	153	2	US-10-104-047-3229	Sequence 3229, Ap
233	7	0.3	156	2	US-09-889-463A-8	Sequence 8, Appli
234	7	0.3	158	2	US-09-270-767-61825	Sequence 61825, A
235	7	0.3	158	2	US-10-104-047-3047	Sequence 3047, Ap
236	7	0.3	161	2	US-09-270-767-59514	Sequence 59514, A
237	7	0.3	162	2	US-09-252-991A-17602	Sequence 17602, A
238	7	0.3	162	2	US-09-252-991A-31660	Sequence 31660, A
239	7	0.3	164	2	US-09-621-976-5191	Sequence 5191, Ap
240	7	0.3	164	2	US-09-605-703B-2190	Sequence 2190, Ap
241	7	0.3	166	2	US-09-252-991A-32785	Sequence 32785, A
242	7	0.3	166	2	US-09-270-767-38629	Sequence 38629, A
243	7	0.3	166	2	US-09-270-767-53846	Sequence 53846, A
244	7	0.3	168	2	US-09-328-352-7072	Sequence 7072, Ap
245	7	0.3	171	2	US-09-252-991A-31864	Sequence 31864, A
246	7	0.3	172	2	US-09-732-210-525	Sequence 525, App
247	7	0.3	175	2	US-09-252-991A-29851	Sequence 29851, A
248	7	0.3	175	2	US-09-270-767-32644	Sequence 32644, A
249	7	0.3	175	2	US-09-270-767-47861	Sequence 47861, A
250	7	0.3	175	2	US-09-248-796A-22789	Sequence 22789, A

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OM protein - protein search, using sw model

Run on: June 26, 2006, 08:33:03 ; Search time 294 Seconds
                                              (without alignments)
                                              3993.646 Million cell updates/sec

Title: US-10-723-361-3
Perfect score: 2568
Sequence: 1 MAISSRLALWEQKIREEDKS..........PGTGRKDDDVASIMKKYLQK 2568

Scoring table: OLIGO
                   Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size :   1

Total number of hits satisfying chosen parameters: 2589342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 250 summaries

Database :   A_Geneseq_8:*
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                   8: geneseqp2004s:*
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                   10: geneseqp2006s:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2568	100.0	2568	5	ABB06333	Abb06333 Human gen
2	2568	100.0	2568	5	AAO17711	Aao17711 Human myo
3	2568	100.0	2568	8	ABM85882	Abm85882 Human GDM
4	1745	68.0	1745	5	ABB06334	Abb06334 Human gen
5	1208	47.0	2063	6	ABP98814	Abp98814 Human str
6	460	17.9	567	7	ADC31353	Adc31353 Human nov
7	457	17.8	457	7	ADM04739	Adm04739 Human pro
8	457	17.8	457	9	AEC87669	Aec87669 Human cDN
9	311	12.1	311	8	ABO60250	Abo60250 Human gen
10	220	8.6	275	4	AAB59528	Aab59528 Human sec
11	207	8.1	207	4	AAB59476	Aab59476 Human sec
12	207	8.1	207	6	ABP99788	Abp99788 Human sec

13	207	8.1	207	6	ABR01281	Abr01281 Human gen
14	207	8.1	207	7	ADC20529	Adc20529 Human sec
15	162	6.3	162	4	ABB32754	Abb32754 Peptide #
16	162	6.3	162	4	AAM26216	Aam26216 Peptide #
17	162	6.3	162	4	ABB18236	Abb18236 Protein #
18	162	6.3	162	5	ABG35586	Abg35586 Human pep
19	153	6.0	153	3	AAB41834	Aab41834 Human ORF
20	101	3.9	111	4	ABG02805	Abg02805 Novel hum
21	58	2.3	205	4	ABG02806	Abg02806 Novel hum
22	52	2.0	52	4	AAM15342	Aam15342 Peptide #
23	52	2.0	52	4	ABB34338	Abb34338 Peptide #
24	52	2.0	52	4	AAM27820	Aam27820 Peptide #
25	52	2.0	52	4	ABB29182	Abb29182 Peptide #
26	52	2.0	52	4	ABB19759	Abb19759 Protein #
27	52	2.0	52	4	AAM67528	Aam67528 Human bon
28	52	2.0	52	4	AAM55135	Aam55135 Human bra
29	52	2.0	52	4	ABG49172	Abg49172 Human liv
30	52	2.0	52	4	AAM03101	Aam03101 Peptide #
31	52	2.0	52	5	ABG37124	Abg37124 Human pep
32	47	1.8	47	8	ABO53932	Abo53932 Human gen
33	43	1.7	43	8	ABO53820	Abo53820 Human gen
34	37	1.4	66	8	ABO53924	Abo53924 Human gen
35	26	1.0	26	10	AEE38616	Aee38616 Human ser
36	24	0.9	29	10	AEE38986	Aee38986 Human ser
37	12	0.5	1524	6	ABU52598	Abu52598 Human NOV
38	12	0.5	1581	5	ABB06336	Abb06336 Human GDM
39	12	0.5	1581	8	ABM85884	Abm85884 Human GDM
40	12	0.5	1906	7	ADE15649	Ade15649 Human str
41	12	0.5	2039	6	AAE32120	Aae32120 Human cyt
42	12	0.5	2042	8	ADS88147	Ads88147 Human pro
43	12	0.5	2067	8	ADN00369	Adn00369 Novel hum
44	10	0.4	232	9	ABM92465	Abm92465 M. xanthu
45	9	0.4	17	8	ADP45574	Adp45574 Pro/Ser r
46	9	0.4	17	9	ADZ07611	Adz07611 NogoA bin
47	9	0.4	20	9	AED42331	Aed42331 Human pro
48	9	0.4	97	6	ABU71088	Abu71088 Human adi
49	9	0.4	128	7	ADE78227	Ade78227 Endometri
50	9	0.4	165	4	AAU65915	Aau65915 Propionib
51	9	0.4	165	6	ABM62434	Abm62434 Propionib
52	9	0.4	166	6	ABU61024	Abu61024 Human ova
53	9	0.4	166	7	ADE78226	Ade78226 Endometri
54	9	0.4	188	4	AAU41582	Aau41582 Propionib
55	9	0.4	188	6	ABM38101	Abm38101 Propionib
56	9	0.4	248	2	AAR31891	Aar31891 T.thermop
57	9	0.4	253	4	ABB65198	Abb65198 Drosophil
58	9	0.4	272	8	ADX90852	Adx90852 Plant ful
59	9	0.4	329	3	AAB58152	Aab58152 Lung canc
60	9	0.4	339	5	ABP41586	Abp41586 Human ova
61	9	0.4	407	8	ADS25108	Ads25108 Bacterial
62	9	0.4	438	7	ADJ68453	Adj68453 Human hea
63	9	0.4	471	9	ADZ99271	Adz99271 S. divers
64	9	0.4	471	9	ADZ99264	Adz99264 S. divers
65	9	0.4	471	9	ADZ99278	Adz99278 S. divers
66	9	0.4	471	9	ADZ99293	Adz99293 S. divers
67	9	0.4	471	9	ADZ99314	Adz99314 S. divers
68	9	0.4	471	9	ADZ99195	Adz99195 S. divers
69	9	0.4	471	9	ADZ99300	Adz99300 S. divers
70	9	0.4	471	9	ADZ99257	Adz99257 S. divers
71	9	0.4	471	9	ADZ99285	Adz99285 S. divers
72	9	0.4	471	9	ADZ99307	Adz99307 S. divers
73	9	0.4	499	5	ABP64950	Abp64950 Human pro

74	9	0.4	522	8	ADS26122	Ads26122 Bacterial
75	9	0.4	568	8	ADS22872	Ads22872 Bacterial
76	9	0.4	606	8	ADS22542	Ads22542 Bacterial
77	9	0.4	606	8	ADS25641	Ads25641 Bacterial
78	9	0.4	620	6	ABU34746	Abu34746 Protein e
79	9	0.4	621	7	ADF30481	Adf30481 Rat angio
80	9	0.4	639	6	ABU36687	Abu36687 Protein e
81	9	0.4	639	6	ABU33985	Abu33985 Protein e
82	9	0.4	642	6	ABR56740	Abr56740 Human sec
83	9	0.4	791	7	ABM86740	Abm86740 Rice abio
84	9	0.4	929	4	ABG09413	Abg09413 Novel hum
85	9	0.4	962	7	ADE78228	Ade78228 Endometri
86	9	0.4	1236	9	ADZ85040	Adz85040 Full-leng
87	9	0.4	1694	5	ABB06335	Abb06335 Human GDM
88	9	0.4	1695	8	ABM85883	Abm85883 Human GDM
89	9	0.4	1851	4	ABG01723	Abg01723 Novel hum
90	9	0.4	1959	5	ABJ10604	Abj10604 Human nov
91	9	0.4	1959	8	ADO09979	Ado09979 Human NOV
92	9	0.4	1959	8	ADO09869	Ado09869 Human NOV
93	9	0.4	1959	9	AEA28591	Aea28591 Chicken m
94	9	0.4	1960	4	AAM78854	Aam78854 Human pro
95	9	0.4	1960	7	ADB70370	Adb70370 PAC 6802
96	9	0.4	1960	7	ADD47946	Add47946 Human Pro
97	9	0.4	1960	8	ADJ37149	Adj37149 Human mal
98	9	0.4	1960	8	ABM82345	Abm82345 Tumour-as
99	9	0.4	1960	8	ADN60283	Adn60283 Human non
100	9	0.4	1960	8	ADT50363	Adt50363 Human non
101	9	0.4	1960	9	ADZ85041	Adz85041 Full-leng
102	9	0.4	1960	9	AEA28585	Aea28585 Human myo
103	9	0.4	1960	9	AEA28589	Aea28589 Mouse myo
104	9	0.4	1960	9	AEC64930	Aec64930 Mouse non
105	9	0.4	1960	9	AEC64932	Aec64932 Human non
106	9	0.4	1960	9	AED11093	Aed11093 Human non
107	9	0.4	1961	9	AEA28587	Aea28587 Rat myosi
108	9	0.4	1963	4	AAM79838	Aam79838 Human pro
109	9	0.4	1972	2	AAW00024	Aaw00024 Smooth mu
110	9	0.4	1976	6	ABU07447	Abu07447 Protein d
111	9	0.4	1976	7	ADE63514	Ade63514 Rat Prote
112	9	0.4	1976	7	ADE63518	Ade63518 Rat Prote
113	9	0.4	1976	9	ADY16758	Ady16758 PRO polyp
114	9	0.4	1976	9	AEC64936	Aec64936 Human non
115	9	0.4	1976	9	AEC64934	Aec64934 Mouse non
116	9	0.4	1988	4	AAM41000	Aam41000 Human pol
117	9	0.4	1988	4	AAM40999	Aam40999 Human pol
118	9	0.4	2143	4	ABG01716	Abg01716 Novel hum
119	8	0.3	19	3	AAB13053	Aab13053 Anchor pe
120	8	0.3	20	5	ABP55501	Abp55501 P1025 pep
121	8	0.3	20	9	AEB44920	Aeb44920 S. mutans
122	8	0.3	21	2	AAW02095	Aaw02095 S. mutans
123	8	0.3	33	4	AAO04814	Aao04814 Human pol
124	8	0.3	33	4	ABG11329	Abg11329 Novel hum
125	8	0.3	40	2	AAW02088	Aaw02088 S. mutans
126	8	0.3	42	8	ADM42908	Adm42908 Human INS
127	8	0.3	42	8	ADM43008	Adm43008 Human INS
128	8	0.3	42	8	ADM42950	Adm42950 Human INS
129	8	0.3	44	4	AAO04929	Aao04929 Human pol
130	8	0.3	50	4	AAU43638	Aau43638 Propionib
131	8	0.3	50	6	ABM40157	Abm40157 Propionib
132	8	0.3	50	9	AED42298	Aed42298 Human pro
133	8	0.3	56	4	AAM89833	Aam89833 Human imm
134	8	0.3	57	2	AAW88986	Aaw88986 Polypepti

135	8	0.3	57	4	ABB51062	Abb51062	Human sec
136	8	0.3	57	6	ABO45319	Abo45319	Novel hum
137	8	0.3	57	7	ABO26799	Abo26799	Protein a
138	8	0.3	62	3	AAB44916	Aab44916	Human sec
139	8	0.3	64	3	AAG02530	Aag02530	Human sec
140	8	0.3	70	2	AAW02094	Aaw02094	S. mutans
141	8	0.3	70	4	AAO02211	Aao02211	Human pol
142	8	0.3	72	5	ABJ10362	Abj10362	Human bre
143	8	0.3	74	4	AAO12182	Aao12182	Human pol
144	8	0.3	75	4	AAO05690	Aao05690	Human pol
145	8	0.3	76	7	ADB75406	Adb75406	Prostate
146	8	0.3	76	7	ADE61186	Ade61186	Rat Prote
147	8	0.3	76	7	ADE61188	Ade61188	Human Pro
148	8	0.3	76	8	ADP24877	Adp24877	PRO polyp
149	8	0.3	77	4	AAO01289	Aao01289	Human pol
150	8	0.3	78	4	AAM18797	Aam18797	Peptide #
151	8	0.3	78	4	ABB37902	Abb37902	Peptide #
152	8	0.3	78	4	AAM31311	Aam31311	Peptide #
153	8	0.3	78	4	ABB23156	Abb23156	Protein #
154	8	0.3	78	4	AAM71034	Aam71034	Human bon
155	8	0.3	78	4	AAM58534	Aam58534	Human bra
156	8	0.3	78	4	ABG52749	Abg52749	Human liv
157	8	0.3	78	5	ABG40825	Abg40825	Human pep
158	8	0.3	83	5	ABP02217	Abp02217	Human ORF
159	8	0.3	87	5	AAU75295	Aau75295	Cytochrom
160	8	0.3	88	4	AAO02124	Aao02124	Human pol
161	8	0.3	94	4	AAO06605	Aao06605	Human pol
162	8	0.3	102	4	AAU32476	Aau32476	Novel hum
163	8	0.3	105	4	ABG15609	Abg15609	Novel hum
164	8	0.3	105	4	ABG15600	Abg15600	Novel hum
165	8	0.3	108	4	AAU64614	Aau64614	Propionib
166	8	0.3	108	6	ABM61133	Abm61133	Propionib
167	8	0.3	109	7	ADM06040	Adm06040	Human pro
168	8	0.3	109	9	AEC88970	Aec88970	Human cDN
169	8	0.3	110	2	AAW02090	Aaw02090	S. mutans
170	8	0.3	121	3	AAG14889	Aag14889	Arabidops
171	8	0.3	124	6	ABP75466	Abp75466	Human sec
172	8	0.3	124	6	ABP75933	Abp75933	Human sec
173	8	0.3	124	7	ADI40596	Adi40596	Human pur
174	8	0.3	130	2	AAW02092	Aaw02092	S. mutans
175	8	0.3	137	4	AAU32730	Aau32730	Novel hum
176	8	0.3	143	3	AAG14888	Aag14888	Arabidops
177	8	0.3	146	8	ADX76720	Adx76720	Plant ful
178	8	0.3	155	5	ADK35111	Adk35111	Novel hum
179	8	0.3	159	3	AAG35191	Aag35191	Zea mays
180	8	0.3	160	8	ADX71048	Adx71048	Plant ful
181	8	0.3	161	5	ABP41851	Abp41851	Human ova
182	8	0.3	169	3	AAG57585	Aag57585	Arabidops
183	8	0.3	169	3	AAG59969	Aag59969	Arabidops
184	8	0.3	173	4	AAU31918	Aau31918	Novel hum
185	8	0.3	173	7	ADB64871	Adb64871	Human pro
186	8	0.3	178	3	AAG59968	Aag59968	Arabidops
187	8	0.3	178	3	AAG57584	Aag57584	Arabidops
188	8	0.3	181	8	ADX92231	Adx92231	Plant ful
189	8	0.3	182	8	ADY11574	Ady11574	Plant ful
190	8	0.3	185	6	ABU94229	Abu94229	Trifolium
191	8	0.3	188	3	AAB44989	Aab44989	Human sec
192	8	0.3	190	2	AAW02087	Aaw02087	S. mutans
193	8	0.3	190	7	ADC86937	Adc86937	Human GPC
194	8	0.3	194	5	ADK36966	Adk36966	Novel hum
195	8	0.3	208	8	ADQ09812	Adq09812	Zebrafish

196	8	0.3	214	2	AAR86913	Aar86913	Cotton fi
197	8	0.3	214	4	ABG00580	Abg00580	Novel hum
198	8	0.3	219	7	ABO79482	Abo79482	Pseudomon
199	8	0.3	220	6	ABU94271	Abu94271	Trifolium
200	8	0.3	222	5	AAU79087	Aau79087	Alfalfa c
201	8	0.3	222	8	ADM32819	Adm32819	Amino aci
202	8	0.3	223	5	AAU79089	Aau79089	Pea chalc
203	8	0.3	244	9	ADZ10566	Adz10566	P. gingiv
204	8	0.3	259	8	ADQ65323	Adq65323	Novel hum
205	8	0.3	262	3	AAB07793	Aab07793	Partial m
206	8	0.3	265	8	ADX93286	Adx93286	Plant ful
207	8	0.3	273	2	AAW23277	Aaw23277	Bordetell
208	8	0.3	274	8	ADN63339	Adn63339	Tobamovir
209	8	0.3	274	8	ADN63284	Adn63284	Tobamovir
210	8	0.3	276	3	AAG58018	Aag58018	Arabidops
211	8	0.3	276	7	ABO63173	Abo63173	Klebsiell
212	8	0.3	282	7	ADB95060	Adb95060	A. thalia
213	8	0.3	286	2	AAW61477	Aaw61477	A. fumiga
214	8	0.3	286	2	AAW88983	Aaw88983	Polypepti
215	8	0.3	286	4	ABB51059	Abb51059	Human sec
216	8	0.3	286	6	ABO45316	Abo45316	Novel hum
217	8	0.3	286	7	ABO26796	Abo26796	Protein a
218	8	0.3	289	3	AAG58017	Aag58017	Arabidops
219	8	0.3	290	8	ADX73222	Adx73222	Plant ful
220	8	0.3	293	3	AAG58016	Aag58016	Arabidops
221	8	0.3	295	5	ABG77197	Abg77197	Selected
222	8	0.3	301	4	ABG07711	Abg07711	Novel hum
223	8	0.3	309	4	ABG03277	Abg03277	Novel hum
224	8	0.3	309	4	ABG15065	Abg15065	Novel hum
225	8	0.3	311	4	ABB59518	Abb59518	Drosophil
226	8	0.3	312	2	AAW02096	Aaw02096	S. mutans
227	8	0.3	315	4	AAB68545	Aab68545	Human GTP
228	8	0.3	315	6	ABP58632	Abp58632	Human lat
229	8	0.3	316	5	ABG97509	Abg97509	Human NOV
230	8	0.3	326	4	ABG00257	Abg00257	Novel hum
231	8	0.3	333	5	ABJ11068	Abj11068	Yeast sel
232	8	0.3	343	7	ABO81799	Abo81799	Pseudomon
233	8	0.3	344	7	ABO61832	Abo61832	Klebsiell
234	8	0.3	351	6	ABR41279	Abr41279	Human DIT
235	8	0.3	365	2	AAW73912	Aaw73912	Mutant E2
236	8	0.3	365	6	ABU45741	Abu45741	Protein e
237	8	0.3	366	6	ABU49718	Abu49718	Protein e
238	8	0.3	369	8	ADT57684	Adt57684	Plant pol
239	8	0.3	372	6	ABU00706	Abu00706	S. pneumo
240	8	0.3	375	2	AAR43664	Aar43664	Ornithine
241	8	0.3	375	2	AAR43663	Aar43663	Ornithine
242	8	0.3	382	8	ADM87614	Adm87614	Human EST
243	8	0.3	390	8	ADN27090	Adn27090	Bacterial
244	8	0.3	399	8	ADN18018	Adn18018	Bacterial
245	8	0.3	414	7	ABO72184	Abo72184	Pseudomon
246	8	0.3	436	4	ABU53062	Abu53062	Human tes
247	8	0.3	437	2	AAR42458	Aar42458	Retinobla
248	8	0.3	437	2	AAW62464	Aaw62464	Transcrip
249	8	0.3	437	2	AAW73913	Aaw73913	E2F1 tran
250	8	0.3	437	3	AAY91046	Aay91046	Human tra

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2006, 06:19:26 ; Search time 947 Seconds
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Title: US-10-723-361-3
Perfect score: 13101
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Scoring table: BLOSUM62
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                    Delop   6.0 , Delext   7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10723361/runat_26062006_061908_27826/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss06p -USER=US10723361_@CGN_1_1_307_@runat_26062006_061908_27826
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
                    1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                    2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                    3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                    4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                    5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                    6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                    7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                    8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                    9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                    10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
              %

Result No.	Score	Query Match	Length	DB	ID	Description
1	13101	100.0	7707	3	US-09-866-108A-2	Sequence 2, Appli
2	13101	100.0	8117	3	US-09-866-108A-1	Sequence 1, Appli
3	7911	60.4	4916	3	US-09-866-108A-5	Sequence 5, Appli
4	4799	36.6	2953	3	US-09-866-108A-4	Sequence 4, Appli
5	2294	17.5	1314	3	US-09-866-108A-15667	Sequence 15667, A
6	2095	16.0	1246	3	US-09-866-108A-15706	Sequence 15706, A
7	1352.5	10.3	6644	3	US-08-875-435B-5	Sequence 5, Appli
8	1330	10.2	6175	3	US-08-875-435B-1	Sequence 1, Appli
9	1323	10.1	6861	3	US-09-949-016-1240	Sequence 1240, Ap
10	1323	10.1	6861	3	US-09-949-016-1241	Sequence 1241, Ap
11	1323	10.1	6861	3	US-09-949-016-1242	Sequence 1242, Ap
12	1316.5	10.0	5835	4	US-09-927-597-1	Sequence 1, Appli
13	1311	10.0	5937	4	US-09-927-597-3	Sequence 3, Appli
14	1292	9.9	7596	3	US-09-023-655-1463	Sequence 1463, Ap
15	1286	9.8	7453	3	US-09-620-312D-248	Sequence 248, App
16	1277	9.7	7501	3	US-09-620-312D-249	Sequence 249, App
17	1267	9.7	5883	3	US-09-949-016-5001	Sequence 5001, Ap
18	1191	9.1	5574	3	US-09-917-254-40	Sequence 40, Appl
19	1175.5	9.0	6008	3	US-09-949-016-5058	Sequence 5058, Ap
20	1169	8.9	6016	3	US-09-949-016-1054	Sequence 1054, Ap
21	1168.5	8.9	6011	3	US-09-949-016-3017	Sequence 3017, Ap
22	1160.5	8.9	6016	3	US-09-949-016-2264	Sequence 2264, Ap
23	1153	8.8	5925	3	US-09-949-016-5233	Sequence 5233, Ap
24	1147	8.8	5992	3	US-09-949-016-546	Sequence 546, App
25	1140	8.7	5992	3	US-09-949-016-2263	Sequence 2263, Ap
26	1081.5	8.3	5661	3	US-08-938-105-2	Sequence 2, Appli
27	870	6.6	500	3	US-09-866-108A-15711	Sequence 15711, A
28	858	6.5	500	3	US-09-866-108A-15750	Sequence 15750, A
29	841	6.4	2535	4	US-09-927-597-13	Sequence 13, Appl
30	834.5	6.4	2556	4	US-09-927-597-11	Sequence 11, Appl
31	822.5	6.3	6396	3	US-09-949-016-3344	Sequence 3344, Ap
32	819.5	6.3	2547	4	US-09-927-597-9	Sequence 9, Appli
33	818.5	6.2	6856	3	US-09-566-921-42	Sequence 42, Appl
34	763	5.8	5919	3	US-08-875-435B-2	Sequence 2, Appli
35	720	5.5	7465	4	US-09-880-107-3357	Sequence 3357, Ap
36	711	5.4	5185	3	US-09-976-594-640	Sequence 640, App
37	695.5	5.3	7787	3	US-09-949-016-964	Sequence 964, App
38	674.5	5.1	7787	3	US-09-949-016-4328	Sequence 4328, Ap
39	651.5	5.0	2316	4	US-09-927-597-7	Sequence 7, Appli
c 40	650	5.0	7066	3	US-09-919-039-362	Sequence 362, App
41	641	4.9	1239	3	US-09-270-767-10388	Sequence 10388, A
42	622.5	4.8	7055	3	US-09-976-594-941	Sequence 941, App
43	607	4.6	2592	3	US-09-248-796A-6509	Sequence 6509, Ap
44	605.5	4.6	8473	3	US-09-172-422-2	Sequence 2, Appli
45	602	4.6	2097	4	US-09-927-597-5	Sequence 5, Appli

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2006, 06:20:34 ; Search time 5733 Seconds
                                                (without alignments)
                                                8256.056 Million cell updates/sec

Title: US-10-723-361-3
Perfect score: 13101
Sequence: 1 MAISSRLALWEQKIREEDKS..........PGTGRKDDDVASIMKKYLQK 2568

Scoring table: BLOSUM62
                     Xgapop 10.0 , Xgapext 0.5
                     Ygapop 10.0 , Ygapext 0.5
                     Fgapop 6.0 , Fgapext 7.0
                     Delop   6.0 , Delext   7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10723361/runat_26062006_061911_27887/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss04
-USER=US10723361_@CGN_1_1_1675_@runat_26062006_061911_27887 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA_Main:*
                     1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                     2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                     3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                     4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                     5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                     6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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                     8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                     9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                     10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                     11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                     12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                     13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                     14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                     15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13101	100.0	7707	3	US-09-866-108-2	Sequence 2, Appli
2	13101	100.0	7707	8	US-10-723-361-2	Sequence 2, Appli
3	13101	100.0	8117	3	US-09-866-108-1	Sequence 1, Appli
4	13101	100.0	8117	8	US-10-723-361-1	Sequence 1, Appli
5	7911	60.4	4916	3	US-09-866-108-5	Sequence 5, Appli
6	7911	60.4	4916	8	US-10-723-361-5	Sequence 5, Appli
7	4799	36.6	2953	3	US-09-866-108-4	Sequence 4, Appli
8	4799	36.6	2953	8	US-10-723-361-4	Sequence 4, Appli
9	3717.5	28.4	7597	16	US-11-122-329-106	Sequence 106, App
10	3715	28.4	7557	8	US-10-473-574-46	Sequence 46, Appl
11	3640.5	27.8	6524	7	US-10-080-334-41	Sequence 41, Appl
12	2561	19.5	1736	7	US-10-108-260A-981	Sequence 981, App
13	2294	17.5	1314	3	US-09-866-108-15667	Sequence 15667, A
14	2294	17.5	1314	8	US-10-723-361-15667	Sequence 15667, A
15	2243.5	17.1	4714	10	US-10-450-763-8089	Sequence 8089, Ap
16	2143.5	16.4	4941	13	US-11-097-143-25895	Sequence 25895, A
17	2113.5	16.1	5121	13	US-11-097-143-40823	Sequence 40823, A
18	2100	16.0	1465	3	US-09-864-761-9685	Sequence 9685, Ap
19	2095	16.0	1246	3	US-09-866-108-15706	Sequence 15706, A
20	2095	16.0	1246	8	US-10-723-361-15706	Sequence 15706, A
21	1620	12.4	934	7	US-10-029-386-25123	Sequence 25123, A
22	1456	11.1	853	3	US-09-864-761-17049	Sequence 17049, A
23	1456	11.1	853	3	US-09-864-761-26093	Sequence 26093, A
24	1456	11.1	853	7	US-10-029-386-24808	Sequence 24808, A
25	1328	10.1	6900	6	US-10-171-311-163	Sequence 163, App
26	1328	10.1	6900	8	US-10-764-425-13	Sequence 13, Appl
27	1328	10.1	6900	15	US-11-000-688-1142	Sequence 1142, Ap
28	1323	10.1	6861	6	US-10-171-311-161	Sequence 161, App
29	1323	10.1	6861	7	US-10-341-434-102	Sequence 102, App
30	1323	10.1	6861	10	US-10-923-035-18	Sequence 18, Appl
31	1318	10.1	6187	10	US-10-995-561-144	Sequence 144, App
32	1318	10.1	6925	10	US-10-995-561-145	Sequence 145, App
33	1316.5	10.0	5835	3	US-09-927-597-1	Sequence 1, Appli
34	1316.5	10.0	5835	10	US-10-486-057-1	Sequence 1, Appli
35	1312.5	10.0	6025	10	US-10-995-561-143	Sequence 143, App
36	1312.5	10.0	6148	10	US-10-995-561-147	Sequence 147, App
37	1312.5	10.0	6886	10	US-10-995-561-149	Sequence 149, App
38	1311	10.0	5937	3	US-09-927-597-3	Sequence 3, Appli
39	1311	10.0	5937	10	US-10-486-057-3	Sequence 3, Appli
40	1307.5	10.0	6185	10	US-10-995-561-146	Sequence 146, App
41	1304.5	10.0	7666	15	US-11-069-834-51	Sequence 51, Appl
42	1297	9.9	7619	15	US-11-069-834-53	Sequence 53, Appl
43	1292	9.9	7596	3	US-09-954-456-2215	Sequence 2215, Ap
44	1292	9.9	7596	8	US-10-641-643-1463	Sequence 1463, Ap
45	1292	9.9	7596	10	US-10-843-641A-5242	Sequence 5242, Ap

```
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OM protein - nucleic search, using frame_plus_p2n model

Run on:           June 26, 2006, 07:28:35 ; Search time 247 Seconds
                                            (without alignments)
                                            3738.543 Million cell updates/sec

Title:            US-10-723-361-3
Perfect score:    13101
Sequence:         1 MAISSRLALWEQKIREEDKS.........PGTGRKDDDVASIMKKYLQK 2568

Scoring table:    BLOSUM62
                  Xgapop 10.0 , Xgapext  0.5
                  Ygapop 10.0 , Ygapext  0.5
                  Fgapop  6.0 , Fgapext  7.0
                  Delop   6.0 , Delext   7.0

Searched:         296510 seqs, 119862409 residues

Total number of hits satisfying chosen parameters:       593020

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10723361/runat_26062006_061914_27955/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03p
-USER=US10723361_@CGN_1_1_45_@runat_26062006_061914_27955 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :        Published_Applications_NA_New:*
                  1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                  2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                  3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                  4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                  5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                  6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                  7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                          %
Result               Query
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No.	Score	Match	Length	DB	ID	Description
1	2561	19.5	1736	7	US-11-293-697-981	Sequence 981, App
2	1016.5	7.8	5787	7	US-11-217-529-76923	Sequence 76923, A
3	733.5	5.6	4725	7	US-11-217-529-78769	Sequence 78769, A
4	723.5	5.5	2943	7	US-11-217-529-4264	Sequence 4264, Ap
5	720	5.5	7465	6	US-10-505-928-311	Sequence 311, App
6	691	5.3	4710	7	US-11-217-529-2497	Sequence 2497, Ap
7	684	5.2	5229	6	US-10-449-902-19325	Sequence 19325, A
8	674	5.1	4236	6	US-10-449-902-18054	Sequence 18054, A
9	584	4.5	3230	6	US-10-449-902-26645	Sequence 26645, A
10	567	4.3	4416	7	US-11-217-529-47	Sequence 47, Appl
11	492	3.8	4044	7	US-11-217-529-81638	Sequence 81638, A
12	489.5	3.7	10211	6	US-10-505-928-326	Sequence 326, App
13	483.5	3.7	9588	6	US-10-505-928-101	Sequence 101, App
14	460	3.5	3117	7	US-11-293-697-856	Sequence 856, App
15	435.5	3.3	2931	7	US-11-217-529-82505	Sequence 82505, A
16	425.5	3.2	3318	7	US-11-217-529-4920	Sequence 4920, Ap
17	411.5	3.1	3813	7	US-11-217-529-77490	Sequence 77490, A
18	392	3.0	5373	7	US-11-217-529-5516	Sequence 5516, Ap
19	383.5	2.9	4455	6	US-10-504-973-70	Sequence 70, Appl
20	370	2.8	2599	7	US-11-293-697-2218	Sequence 2218, Ap
21	368.5	2.8	5658	7	US-11-217-529-6026	Sequence 6026, Ap
22	365.5	2.8	7561	7	US-11-289-102-42	Sequence 42, Appl
23	362	2.8	1450	6	US-10-449-902-26422	Sequence 26422, A
24	356.5	2.7	3270	6	US-10-480-962-24	Sequence 24, Appl
25	355.5	2.7	1797	7	US-11-217-529-4576	Sequence 4576, Ap
26	345.5	2.6	2757	7	US-11-334-351-1	Sequence 1, Appli
27	345.5	2.6	3720	6	US-10-449-902-17102	Sequence 17102, A
28	336.5	2.6	5040	7	US-11-217-529-77055	Sequence 77055, A
29	335	2.6	3044	7	US-11-293-697-2049	Sequence 2049, Ap
30	330.5	2.5	5028	7	US-11-217-529-5947	Sequence 5947, Ap
31	330.5	2.5	7434	6	US-10-471-571A-2277	Sequence 2277, Ap
32	328.5	2.5	2490	6	US-10-449-902-462	Sequence 462, App
33	326	2.5	1980	7	US-11-293-697-2304	Sequence 2304, Ap
34	324.5	2.5	4236	6	US-10-449-902-12608	Sequence 12608, A
35	319.5	2.4	12515	6	US-10-505-928-358	Sequence 358, App
36	314.5	2.4	7430	6	US-10-559-415-1	Sequence 1, Appli
37	310	2.4	4925	7	US-11-289-102-97	Sequence 97, Appl
38	308.5	2.4	7268	6	US-10-559-415-189	Sequence 189, App
39	306.5	2.3	2607	7	US-11-217-529-4263	Sequence 4263, Ap
40	304.5	2.3	1684	6	US-10-953-349-20040	Sequence 20040, A
41	304.5	2.3	3069	7	US-11-293-697-1126	Sequence 1126, Ap
42	303.5	2.3	2804	6	US-10-449-902-16474	Sequence 16474, A
43	303	2.3	2479	7	US-11-293-697-1966	Sequence 1966, Ap
44	303	2.3	3943	6	US-10-449-902-16723	Sequence 16723, A
45	301.5	2.3	3307	7	US-11-293-697-1453	Sequence 1453, Ap

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OM protein - protein search, using sw model

Run on:          June 26, 2006, 08:17:47 ; Search time 71 Seconds
                                            (without alignments)
                                            3480.065 Million cell updates/sec

Title:           US-10-723-361-3
Perfect score:   13101
Sequence:        1 MAISSRLALWEQKIREEDKS.........PGTGRKDDDVASIMKKYLQK 2568

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283416 seqs; 96216763 residues

Total number of hits satisfying chosen parameters:       283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_80:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
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                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1319	10.1	1972	1	A41604	myosin heavy chain
2	1319	10.1	1972	2	JC5420	smooth muscle myos
3	1317.5	10.1	1938	2	JC5421	smooth muscle myos
4	1305.5	10.0	1979	1	S03166	myosin heavy chain
5	1291	9.9	2007	1	B43402	myosin heavy chain
6	1280.5	9.8	1976	2	A59252	myosin heavy chain
7	1273	9.7	1961	1	A61231	myosin heavy chain
8	1268	9.7	1999	1	S21801	myosin heavy chain
9	1256	9.6	1992	2	A47297	myosin heavy chain
10	1251.5	9.6	1964	2	A59282	nonmuscle myosin I
11	1244.5	9.5	2017	1	A36014	myosin heavy chain
12	1230.5	9.4	2057	2	S61477	myosin II heavy ch
13	1216.5	9.3	1959	1	A33977	myosin heavy chain
14	1206	9.2	1956	2	T16416	hypothetical prote
15	1184.5	9.0	1938	1	A40997	myosin heavy chain
16	1179.5	9.0	1937	2	I38055	myosin heavy chain
17	1175.5	9.0	2116	2	A26655	myosin heavy chain
18	1175	9.0	1940	2	A59287	myosin heavy chain

19	1170	8.9	1935	1	A37102	myosin beta heavy
20	1169	8.9	1935	1	S06006	myosin beta heavy
21	1168	8.9	1940	2	A29320	myosin heavy chain
22	1163	8.9	1931	2	A59234	slow myosin heavy
23	1161	8.9	1935	2	A59286	myosin heavy chain
24	1161	8.9	1940	1	A24922	myosin heavy chain
25	1159.5	8.9	1939	2	I48175	myosin heavy chain
26	1158.5	8.8	1939	1	A46762	myosin alpha heavy
27	1158.5	8.8	1940	1	S04090	myosin heavy chain
28	1151.5	8.8	1938	1	JX0178	myosin heavy chain
29	1145	8.7	1934	2	I48153	myosin heavy chain
30	1138	8.7	1938	2	I49464	alpha cardiac myos
31	1136	8.7	1938	1	S06005	myosin alpha heavy
32	1131	8.6	1938	2	A59293	skeletal myosin he
33	1125	8.6	2020	2	T21174	hypothetical prote
34	1102	8.4	1509	1	A27224	myosin heavy chain
35	1087.5	8.3	1927	2	A59236	embryonic muscle m
36	1079	8.2	1974	2	T30010	hypothetical prote
37	1067.5	8.1	1957	2	A59294	skeletal myosin -
38	1067.5	8.1	2139	2	T18296	myosin heavy chain
39	1066.5	8.1	1957	2	A45627	myosin heavy chain
40	1045	8.0	1992	1	S02771	myosin heavy chain
41	1033	7.9	1963	1	MWKW	myosin heavy chain
42	1020.5	7.8	1928	2	S46773	myosin heavy chain
43	1003.5	7.7	2385	2	A32491	myosin heavy chain
44	1003.5	7.7	2411	2	B32491	myosin heavy chain
45	989.5	7.6	1526	2	T41522	myosin ii - fissio

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2006, 06:19:23 ; Search time 23428 Seconds
                                               (without alignments)
                                               9194.181 Million cell updates/sec

Title: US-10-723-361-3
Perfect score: 13101
Sequence: 1 MAISSRLALWEQKIREEDKS..........PGTGRKDDDVASIMKKYLQK 2568

Scoring table: BLOSUM62
                    Xgapop 10.0 , Xgapext 0.5
                    Ygapop 10.0 , Ygapext 0.5
                    Fgapop 6.0 , Fgapext 7.0
                    Delop   6.0 , Delext   7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10723361/runat_26062006_061906_27793/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03h
-USER=US10723361_@CGN_1_1_6323_@runat_26062006_061906_27793 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   EST:*
                    1: gb_est1:*
                    2: gb_est3:*
                    3: gb_est4:*
                    4: gb_est5:*
                    5: gb_est6:*
                    6: gb_htc:*
                    7: gb_est2:*
                    8: gb_est7:*
                    9: gb_est8:*
                    10: gb_est9:*
                    11: gb_gss1:*
                    12: gb_gss2:*
                    13: gb_gss3:*
                    14: gb_gss4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8851	67.6	6243	14	DQ038526	DQ038526 Homo sapi
2	5899	45.0	6243	14	DQ038527	DQ038527 Pan trogl
3	3704.5	28.3	7525	6	CR933614	CR933614 Homo sapi
4	3620.5	27.6	6340	6	AK147584	AK147584 Mus muscu
5	3618	27.6	6179	6	AK171342	AK171342 Mus muscu
6	3544	27.1	6129	14	DQ054174	DQ054174 Homo sapi
7	3343	25.5	2833	6	AK016515	AK016515 Mus muscu
8	3317	25.3	2324	6	CR749556	CR749556 Homo sapi
9	2608	19.9	2512	6	AK077135	AK077135 Mus muscu
10	2166.5	16.5	6129	14	DQ054175	DQ054175 Pan trogl
11	1912	14.6	2684	6	AK137574	AK137574 Mus muscu
12	1595	12.2	2133	6	CR615876	CR615876 full-leng
13	1349	10.3	859	5	CF551892	CF551892 AGENCOURT
14	1306.5	10.0	7762	6	AK147567	AK147567 Mus muscu
15	1272	9.7	903	10	DV932484	DV932484 LB03025.C
16	1268.5	9.7	7365	6	AK147407	AK147407 Mus muscu
17	1262.5	9.6	6275	6	AK029236	AK029236 Mus muscu
18	1262	9.6	7410	6	AK147211	AK147211 Mus muscu
19	1260.5	9.6	7371	6	AK147208	AK147208 Mus muscu
20	1260.5	9.6	7372	6	AK147430	AK147430 Mus muscu
21	1259.5	9.6	7350	6	AK147222	AK147222 Mus muscu
22	1259.5	9.6	7354	6	AK147203	AK147203 Mus muscu
23	1259.5	9.6	7359	6	AK147223	AK147223 Mus muscu
24	1259.5	9.6	7362	6	AK147209	AK147209 Mus muscu
25	1259.5	9.6	7362	6	AK147233	AK147233 Mus muscu
26	1259.5	9.6	7363	6	AK147206	AK147206 Mus muscu
27	1259.5	9.6	7366	6	AK147210	AK147210 Mus muscu
28	1259.5	9.6	7366	6	AK147235	AK147235 Mus muscu
29	1259.5	9.6	7366	6	AK147296	AK147296 Mus muscu
30	1259	9.6	7304	6	AK147216	AK147216 Mus muscu
31	1259	9.6	7309	6	AK147221	AK147221 Mus muscu
32	1259	9.6	7353	6	AK147215	AK147215 Mus muscu
33	1248	9.5	941	3	BQ931968	BQ931968 AGENCOURT
34	1192.5	9.1	730	4	BX646937	BX646937 DKFZp779E
35	1188.5	9.1	6054	6	AK169198	AK169198 Mus muscu
36	1188.5	9.1	6054	6	AK169371	AK169371 Mus muscu
37	1188.5	9.1	6055	6	AK147031	AK147031 Mus muscu
38	1178.5	9.0	5814	14	DQ052207	DQ052207 Homo sapi
39	1177.5	9.0	6062	6	HSM802948	BX510904 Homo sapi
40	1176.5	9.0	4465	6	AK137226	AK137226 Mus muscu
41	1168	8.9	5495	14	AY407957	AY407957 Mus muscu
42	1166	8.9	5504	14	AY407955	AY407955 Homo sapi
43	1160.5	8.9	5820	14	DQ029772	DQ029772 Homo sapi
44	1156.5	8.8	969	4	BY716194	BY716194 BY716194
45	1133	8.6	5838	14	DQ037834	DQ037834 Homo sapi

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OM protein - protein search, using sw model

Run on:          June 26, 2006, 08:12:32 ; Search time 460 Seconds
                                              (without alignments)
                                           5164.000 Million cell updates/sec


Title:           US-10-723-361-3
Perfect score:   13101
Sequence:        1 MAISSRLALWEQKIREEDKS..........PGTGRKDDDVASIMKKYLQK 2568


Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5


Searched:        2849598 seqs, 925015592 residues


Total number of hits satisfying chosen parameters:      2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :       UniProt_7.2:*
                 1:  uniprot_sprot:*
                 2:  uniprot_trembl:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13059.5	99.7	2567	1	MY18B_HUMAN	Q8iug5 homo sapien
2	13037	99.5	2566	2	Q5TF64_HUMAN	Q5tf64 homo sapien
3	4212	32.2	1972	2	Q4S1U4_TETNG	Q4s1u4 tetraodon n
4	3668.5	28.0	2046	2	Q5W9G1_HUMAN	Q5w9g1 homo sapien
5	3668.5	28.0	2054	1	MY18A_HUMAN	Q92614 homo sapien
6	3653	27.9	2039	2	Q5H9U3_HUMAN	Q5h9u3 homo sapien
7	3624.5	27.7	1715	2	Q5W9F9_HUMAN	Q5w9f9 homo sapien
8	3600.5	27.5	2035	1	MY18A_MOUSE	Q9jmh9 mus musculu
9	3600.5	27.5	2035	2	Q5SYP0_MOUSE	Q5syp0 mus musculu
10	3600	27.5	2050	2	Q5SYN9_MOUSE	Q5syn9 mus musculu
11	3572	27.3	1700	2	Q3TBB2_MOUSE	Q3tbb2 mus musculu
12	3571.5	27.3	1722	2	Q3UH48_MOUSE	Q3uh48 mus musculu
13	3462	26.4	1998	2	Q5SYP1_MOUSE	Q5syp1 mus musculu
14	3322	25.4	1581	2	Q5QD01_HUMAN	Q5qd01 homo sapien
15	3317	25.3	668	2	Q68D67_HUMAN	Q68d67 homo sapien
16	3182	24.3	2754	2	Q4T1L1_TETNG	Q4t1l1 tetraodon n
17	3112.5	23.8	745	2	Q9D4I1_MOUSE	Q9d4i1 mus musculu
18	2327	17.8	457	2	Q8N903_HUMAN	Q8n903 homo sapien
19	2197	16.8	2028	2	Q9VEZ0_DROME	Q9vez0 drosophila
20	2165	16.5	2209	2	Q8INC4_DROME	Q8inc4 drosophila

21	2156.5	16.5	2089	2	Q8INC3_DROME	Q8inc3 drosophila
22	1973.5	15.1	1858	2	Q5TVZ3_ANOGA	Q5tvz3 anopheles g
23	1933	14.8	1909	2	Q7QHD4_ANOGA	Q7qhd4 anopheles g
24	1911.5	14.6	873	2	Q3UV60_MOUSE	Q3uv60 mus musculu
25	1699	13.0	1357	2	Q4S8N2_TETNG	Q4s8n2 tetraodon n
26	1320	10.1	1972	1	MYH11_RABIT	P35748 oryctolagus
27	1319	10.1	1972	1	MYH11_MOUSE	O08638 mus musculu
28	1314.5	10.0	1972	2	Q8R384_MOUSE	Q8r384 mus musculu
29	1313.5	10.0	1984	2	Q69ZX3_MOUSE	Q69zx3 mus musculu
30	1309	10.0	2016	2	Q7PF90_ANOGA	Q7pf90 anopheles g
31	1304.5	10.0	1978	1	MYH11_CHICK	P10587 gallus gall
32	1302.5	9.9	1938	2	Q3MIV8_HUMAN	Q3miv8 homo sapien
33	1302.5	9.9	1972	1	MYH11_HUMAN	P35749 homo sapien
34	1297	9.9	1997	2	Q02015_CHICK	Q02015 gallus gall
35	1296	9.9	1945	2	Q3MNF0_HUMAN	Q3mnf0 homo sapien
36	1296	9.9	1979	2	Q3MNF1_HUMAN	Q3mnf1 homo sapien
37	1291	9.9	2007	2	Q789A4_CHICK	Q789a4 gallus gall
38	1290	9.8	2018	2	Q4LE45_HUMAN	Q4le45 homo sapien
39	1289.5	9.8	1976	2	Q789A6_CHICK	Q789a6 gallus gall
40	1288	9.8	2007	2	Q5SV64_MOUSE	Q5sv64 mus musculu
41	1284.5	9.8	2013	2	Q3UH59_MOUSE	Q3uh59 mus musculu
42	1283.5	9.8	1986	2	Q789A5_CHICK	Q789a5 gallus gall
43	1280.5	9.8	1976	1	MYH10_HUMAN	P35580 homo sapien
44	1280.5	9.8	1976	1	MYH10_MOUSE	Q61879 mus musculu
45	1272.5	9.7	1976	1	MYH10_RAT	Q9jlt0 rattus norv

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 25, 2006, 14:53:11 ; Search time 8337 Seconds
                                            (without alignments)
                                            5677.339 Million cell updates/sec

Title: US-10-723-361-3
Perfect score: 13101
Sequence: 1 MAISSRLALWEQKIREEDKS..........PGTGRKDDDVASIMKKYLQK 2568

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext   0.5
                 Ygapop 10.0 , Ygapext   0.5
                 Fgapop 6.0 , Fgapext   7.0
                 Delop   6.0 , Delext   7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-THR=4 -MODEL=frame+_p2n.model -DEV=SOFT
-Q=/abss/ABSSWEB_beta_spool/US10723361/runat_23072006_172625_18748/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=0 -MINLEN=0
-MAXLEN=2000000000 -MINDBSEQLEN=1 -HOST=ad1
-USER=US10723361_@CGN_1_1_6147_@runat_23072006_172625_18748 -NCPU=6 -NO_MMAP
-NEG_SCORES=0 -WAIT -LONGLOG -MINDIST=0 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA_Main:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
                 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13101	100.0	7707	3	US-09-866-108-2	Sequence 2, Appli
2	13101	100.0	7707	8	US-10-723-361-2	Sequence 2, Appli
3	13101	100.0	8117	3	US-09-866-108-1	Sequence 1, Appli
4	13101	100.0	8117	8	US-10-723-361-1	Sequence 1, Appli
5	7911	60.4	4916	3	US-09-866-108-5	Sequence 5, Appli
6	7911	60.4	4916	8	US-10-723-361-5	Sequence 5, Appli
7	4799	36.6	2953	3	US-09-866-108-4	Sequence 4, Appli
8	4799	36.6	2953	8	US-10-723-361-4	Sequence 4, Appli
9	3730	28.5	7597	16	US-11-122-329-106	Sequence 106, App
10	3727.5	28.5	7557	8	US-10-473-574-46	Sequence 46, Appl
11	3645.5	27.8	6524	7	US-10-080-334-41	Sequence 41, Appl
12	2561	19.5	1736	7	US-10-108-260A-981	Sequence 981, App
13	2294	17.5	1314	3	US-09-866-108-15667	Sequence 15667, A
14	2294	17.5	1314	8	US-10-723-361-15667	Sequence 15667, A
15	2243.5	17.1	4714	10	US-10-450-763-8089	Sequence 8089, Ap
16	2143.5	16.4	4941	13	US-11-097-143-25895	Sequence 25895, A
17	2113.5	16.1	5121	13	US-11-097-143-40823	Sequence 40823, A
18	2100	16.0	1465	3	US-09-864-761-9685	Sequence 9685, Ap
19	2095	16.0	1246	3	US-09-866-108-15706	Sequence 15706, A
20	2095	16.0	1246	8	US-10-723-361-15706	Sequence 15706, A
21	1620	12.4	934	7	US-10-029-386-25123	Sequence 25123, A
22	1456	11.1	853	3	US-09-864-761-17049	Sequence 17049, A
23	1456	11.1	853	3	US-09-864-761-26093	Sequence 26093, A
24	1456	11.1	853	7	US-10-029-386-24808	Sequence 24808, A
25	1350.5	10.3	6900	6	US-10-171-311-163	Sequence 163, App
26	1350.5	10.3	6900	8	US-10-764-425-13	Sequence 13, Appl
27	1350.5	10.3	6900	15	US-11-000-688-1142	Sequence 1142, Ap
28	1349.5	10.3	6861	6	US-10-171-311-161	Sequence 161, App
29	1349.5	10.3	6861	7	US-10-341-434-102	Sequence 102, App
30	1349.5	10.3	6861	10	US-10-923-035-18	Sequence 18, Appl
31	1343	10.3	6187	10	US-10-995-561-144	Sequence 144, App
32	1343	10.3	6925	10	US-10-995-561-145	Sequence 145, App
33	1340.5	10.2	6148	10	US-10-995-561-147	Sequence 147, App
34	1340.5	10.2	6886	10	US-10-995-561-149	Sequence 149, App
35	1336.5	10.2	6025	10	US-10-995-561-143	Sequence 143, App
36	1334.5	10.2	5937	3	US-09-927-597-3	Sequence 3, Appli
37	1334.5	10.2	5937	10	US-10-486-057-3	Sequence 3, Appli
38	1333	10.2	5835	3	US-09-927-597-1	Sequence 1, Appli
39	1333	10.2	5835	10	US-10-486-057-1	Sequence 1, Appli
40	1332.5	10.2	6185	10	US-10-995-561-146	Sequence 146, App
41	1319	10.1	7666	15	US-11-069-834-51	Sequence 51, Appl
42	1313.5	10.0	11065	6	US-10-116-802-14	Sequence 14, Appl
43	1306.5	10.0	7619	15	US-11-069-834-53	Sequence 53, Appl
44	1301.5	9.9	7596	3	US-09-954-456-2215	Sequence 2215, Ap
45	1301.5	9.9	7596	8	US-10-641-643-1463	Sequence 1463, Ap